

(1) GENERAL INFORMATION:

(i) APPLICANT: Choi et. al.

(ii) TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines

(iii) NUMBER OF SEQUENCES: 452

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Human Genome Sciences, Inc.

(B) STREET: 9410 Key West Avenue

(C) CITY: Rockville

(D) STATE: Maryland

(E) COUNTRY: USA

(F) ZIP: 20850

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

(B) COMPUTER: HP Vectra 486/33

(C) OPERATING SYSTEM: MSDOS version 6.2

(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Brookes, A. Anders
 (B) REGISTRATION NUMBER: 36,373
 (C) REFERENCE/DOCKET NUMBER: PB340P2

(vi) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (301) 309-8504
 (B) TELEFAX: (301) 309-8512

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1999 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

71130

TAAAATCTAC GACAATAAAA ATCAACTCAT TGCTGACTTG GGTTCCTGAAC GCCGCGTCAA	60
TGCCCAAGCT AATGATATTC CCACAGATTT GGTAAAGGCA ATCGTTTCTA TCGAAGACCA	120
TCGCTTCTTC GACCACAGGG GGATTGATAC CATCCGTATC CTGGGAGCTT TCTTGCGCAA	180
TCTGCAAAGC AATTCCCTCC AAGGTGGATC AACTCTCACC CAACAGTTGA TTAAGTTGAC	240
TTACTTTTCA ACTTCGACTT CCGACCAGAC TATTTCTCGT AAGGCTCAGG AAGCTTGGTT	300
AGCGATTTCAG TTAGAACAAA AAGCAACCAA GCAAGAAATC TTGACCTACT ATATAAATAA	360
GGTCTACATG TCTAATGGGA ACTATGGAAT GCAGACAGCA GCTCAAAACT ACTATGGTAA	420
AGACCTCAAT AATTAAAGTT TACCTCAGTT AGCCTTGCTG GCTGGAATGC CTCAGGCACC	480
AAACCAATAT GACCCCTATT CACATCCAGA AGCAGCCCAA GACCGCCGAA ACTTGGTCTT	540
ATCTGAAATG AAAAATCAAG GCTACATCTC TGCTGAACAG TATGAGAAAG CAGTCAATAC	600
ACCAATTACT GATGGACTAC AAAGTCTCAA ATCAGCAAGT AATTACCCTG CTTACATGGA	660
TAATTACCTC AAGGAAGTCA TCAATCAAGT TGAAGAAGAA ACAGGCTATA ACCTACTCAC	720
AACTGGGATG GATGTCTACA CAAATGTAGA CCAAGAAGCT CAAAAACATC TGTGGGATAT	780
TTACAATACA GACGAATACG TTGCCTATCC AGACGATGAA TTGCAAGTCG CTCTACCAT	840

TGTTCATGTT TCTAACGGTA AAGTCATTGC CCAGCTAGGA GCACGCCATC AGTCAAGTAA 900
 TGTTCCTTC GGAATTAACC AAGCAGTAGA AACAAACCGC GACTGGGGAT CAACTATGAA 960
 ACCGATCACA GACTATGCTC CTGCCTTGGA GTACGGTGTC TACGATTCAA CTGCTACTAT 1020
 CGTTCACGAT GAGCCCTATA ACTACCCTGG GACAAATACT CCTGTTTATA ACTGGGATAG 1080
 GGGCTACTTT GGCAACATCA CCTTGCAATA CGCCCTGCAA CAATCGCGAA ACGTCCAGC 1140
 CGTGGAACT CTAAACAAGG TCGGACTCAA CCGCGCCAAG ACTTTCCTAA ATGGTCTAGG 1200
 AATCGACTAC CCAAGTATTC ACTACTCAA TGCCATTTCAGTAACACAA CCGAATCAGA 1260
 CAAAAAATAT GGAGCAAGTA GTGAAAAGAT GGCTGCTGCT TACGCTGCCT TTGCAAATGG 1320
 TGGAACTTAC TATAAACCAA TGTATATCCA TAAAGTCGTC TTTAGTGATG GGAGTGAAAA 1380
 AGAGTTCTCT AATGTCGGAA CTCGTGCCAT GAAGGAAACG ACAGCCTATA TGATGACCGA 1440
 CATGATGAAA ACAGTCTTGA CTTATGGAAC TGGACGAAAT GCCTATCTTG CTTGGCTCCC 1500
 TCAGGCTGGT AAAACAGGAA CCTCTAACTA TACAGACGAG GAAATTGAAA ACCACATCAA 1560
 GACCTCTCAA TTTGTAGCAC CTGATGAACT ATTTGCTGGC TATACGCGTA AATATTCAAT 1620
 GGCTGTATGG ACAGGCTATT CTAACCGTCT GACACCACTT GTAGGCAATG GCCTTACGGT 1680
 CGTGCCAAA GTTTACCGCT CTATGATGAC CTACCTGTCT GAAGGAAGCA ATCCAGAAGA 1740
 TTGGAATATA CCAGAGGGGC TCTACAGAAA TGGAGAATTC GTATTTAAAA ATGGTGCTCG 1800
 TTCTACGTGG AACTCACCTG CTCCACAACA ACCCCATCA ACTGAAAGTT CAAGCTCATC 1860
 ATCAGATAGT TCAACTTCAC AGTCTAGCTC AACCACTCCA AGCACAAATA ATAGTACGAC 1920
 TACCAATCCT AACAAATA CGCAACAATC AAATACAACC CCTGATCAAC AAAATCAGAA 1980
 TCCTCAACCA GCACAACCA 1999

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Lys Ile Tyr Asp Asn Lys Asn Gln Leu Ile Ala Asp Leu Gly Ser Glu
 1 5 10 15

Arg Arg Val Asn Ala Gln Ala Asn Asp Ile Pro Thr Asp Leu Val Lys
 20 25 30

Ala Ile Val Ser Ile Glu Asp His Arg Phe Phe Asp His Arg Gly Ile
 35 40 45

Asp Thr Ile Arg Ile Leu Gly Ala Phe Leu Arg Asn Leu Gln Ser Asn
 50 55 60
 Ser Leu Gln Gly Gly Ser Thr Leu Thr Gln Gln Leu Ile Lys Leu Thr
 65 70 75 80
 Tyr Phe Ser Thr Ser Thr Ser Asp Gln Thr Ile Ser Arg Lys Ala Gln
 85 90 95
 Glu Ala Trp Leu Ala Ile Gln Leu Glu Gln Lys Ala Thr Lys Gln Glu
 100 105 110
 Ile Leu Thr Tyr Tyr Ile Asn Lys Val Tyr Met Ser Asn Gly Asn Tyr
 115 120 125
 Gly Met Gln Thr Ala Ala Gln Asn Tyr Tyr Gly Lys Asp Leu Asn Asn
 130 135 140
 Leu Ser Leu Pro Gln Leu Ala Leu Leu Ala Gly Met Pro Gln Ala Pro
 145 150 155 160
 Asn Gln Tyr Asp Pro Tyr Ser His Pro Glu Ala Ala Gln Asp Arg Arg
 165 170 175
 Asn Leu Val Leu Ser Glu Met Lys Asn Gln Gly Tyr Ile Ser Ala Glu
 180 185 190
 Gln Tyr Glu Lys Ala Val Asn Thr Pro Ile Thr Asp Gly Leu Gln Ser
 195 200 205
 Leu Lys Ser Ala Ser Asn Tyr Pro Ala Tyr Met Asp Asn Tyr Leu Lys
 210 215 220
 Glu Val Ile Asn Gln Val Glu Glu Glu Thr Gly Tyr Asn Leu Leu Thr
 225 230 235 240
 Thr Gly Met Asp Val Tyr Thr Asn Val Asp Gln Glu Ala Gln Lys His
 245 250 255
 Leu Trp Asp Ile Tyr Asn Thr Asp Glu Tyr Val Ala Tyr Pro Asp Asp
 260 265 270
 Glu Leu Gln Val Ala Ser Thr Ile Val Asp Val Ser Asn Gly Lys Val
 275 280 285
 Ile Ala Gln Leu Gly Ala Arg His Gln Ser Ser Asn Val Ser Phe Gly
 290 295 300
 Ile Asn Gln Ala Val Glu Thr Asn Arg Asp Trp Gly Ser Thr Met Lys
 305 310 315 320
 Pro Ile Thr Asp Tyr Ala Pro Ala Leu Glu Tyr Gly Val Tyr Asp Ser
 325 330 335
 Thr Ala Thr Ile Val His Asp Glu Pro Tyr Asn Tyr Pro Gly Thr Asn
 340 345 350
 Thr Pro Val Tyr Asn Trp Asp Arg Gly Tyr Phe Gly Asn Ile Thr Leu
 355 360 365
 Gln Tyr Ala Leu Gln Gln Ser Arg Asn Val Pro Ala Val Glu Thr Leu
 370 375 380

Asn Lys Val Gly Leu Asn Arg Ala Lys Thr Phe Leu Asn Gly Leu Gly
 385 390 395 400
 Ile Asp Tyr Pro Ser Ile His Tyr Ser Asn Ala Ile Ser Ser Asn Thr
 405 410 415
 Thr Glu Ser Asp Lys Lys Tyr Gly Ala Ser Ser Glu Lys Met Ala Ala
 420 425 430
 Ala Tyr Ala Ala Phe Ala Asn Gly Gly Thr Tyr Tyr Lys Pro Met Tyr
 435 440 445
 Ile His Lys Val Val Phe Ser Asp Gly Ser Glu Lys Glu Phe Ser Asn
 450 455 460
 Val Gly Thr Arg Ala Met Lys Glu Thr Thr Ala Tyr Met Met Thr Asp
 465 470 475 480
 Met Met Lys Thr Val Leu Thr Tyr Gly Thr Gly Arg Asn Ala Tyr Leu
 485 490 495
 Ala Trp Leu Pro Gln Ala Gly Lys Thr Gly Thr Ser Asn Tyr Thr Asp
 500 505 510
 Glu Glu Ile Glu Asn His Ile Lys Thr Ser Gln Phe Val Ala Pro Asp
 515 520 525
 Glu Leu Phe Ala Gly Tyr Thr Arg Lys Tyr Ser Met Ala Val Trp Thr
 530 535 540
 Gly Tyr Ser Asn Arg Leu Thr Pro Leu Val Gly Asn Gly Leu Thr Val
 545 550 555 560
 Ala Ala Lys Val Tyr Arg Ser Met Met Thr Tyr Leu Ser Glu Gly Ser
 565 570 575
 Asn Pro Glu Asp Trp Asn Ile Pro Glu Gly Leu Tyr Arg Asn Gly Glu
 580 585 590
 Phe Val Phe Lys Asn Gly Ala Arg Ser Thr Trp Asn Ser Pro Ala Pro
 595 600 605
 Gln Gln Pro Pro Ser Thr Glu Ser Ser Ser Ser Ser Ser Asp Ser Ser
 610 615 620
 Thr Ser Gln Ser Ser Ser Thr Thr Pro Ser Thr Asn Asn Ser Thr Thr
 625 630 635 640
 Thr Asn Pro Asn Asn Asn Thr Gln Gln Ser Asn Thr Thr Pro Asp Gln
 645 650 655
 Gln Asn Gln Asn Pro Gln Pro Ala Gln Pro
 660 665

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AAATTACAAT ACGGACTATG AATTGACCTC TGGAGAAAAA TTACCTCTTC CTAAAGAGAT 60
 TTCAGGTTAC ACTTATATTG GATATATCAA AGAGGGAAAA ACGACTTCTG AGTCTGAAGT 120
 AAGTAATCAA AAGAGTTTCAG TTGCCACTCC TACAAAACAA CAAAAGGTGG ATTATAATGT 180
 TACACCGAAT TTTGTAGACC ATCCATCAAC AGTACAAGCT ATTCAGGAAC AAACACCTGT 240
 TTCTTCAACT AAGCCGACAG AAGTTCAAGT AGTTGAAAAA CCTTTCTCTA CTGAATTAAT 300
 CAATCCAAGA AAAGAAGAGA AACAATCTTC AGATTCTCAA GAACAATTAG CCGAACATAA 360
 GAATCTAGAA ACGAAGAAAG AGGAGAAGAT TTCTCCAAAA GAAAAGACTG GGGTAAATAC 420
 ATTAAATCCA CAGGATGAAG TTTTATCAGG TCAATTGAAC AAACCTGAAC TCTTATATCG 480
 TGAGGAAACT ATGGAGACAA AAATAGATTT TCAAGAAGAA ATTCAAGAAA ATCCTGATTT 540
 AGCTGAAGGA ACTGTAAGAG TAAAACAAGA AGGTAAATTA GGTAAGAAAG TTGAAATCGT 600
 CAGAATATTC TCTGTAAACA AGGAAGAAGT TTCGCGAGAA ATTGTTTCAA CTTCACGAC 660
 TCGCCTAGT CCAAGAATAG TCGAAAAAGG TACTAAAAAA ACTCAAGTTA TAAAGGAACA 720
 ACCTGAGACT GGTGTAGAAC ATAAGGACGT ACAGTCTGGA GCTATTGTGTG AACCCGCAAT 780
 TCAGCCTGAG TTGCCCAGAG CTGTAGTAAG TGACAAAGGC GAACCAGAAG TTCAACCTAC 840
 ATTACCCGAA GCAGTTGTGA CCGACAAAGG TGAGACTGAG GTTCAACCAG AGTCGCCAGA 900
 TACTGTGGTA AGTGATAAAG GTGAACCAGA GCAGGTAGCA CCGCTTCCAG AATATAAGGG 960
 TAATATTGAG CAAGTAAAAC CTGAAACTCC GGTGAGAAG ACCAAAGAAC AAGGTCCAGA 1020
 AAAAAGTAA GAAGTTCCAG TAAAACCAAC AGAAGAAACA CCAGTAAATC CAAATGAAGG 1080
 TACTACAGAA GGAACCTCAA TTCAAGAAGC AGAAAATCCA GTTCAACCTG CAGAAGAATC 1140
 AACACGAAT TCAGAGAAAG TATCACCAGA TACATCTAGC AAAAATACTG GGGAAGTGT 1200
 CAGTAATCCT AGTGATTCGA CAACCTCAGT TGGAGAATCA AATAAACAG AACATAATGA 1260
 CTCTAAAAAT GAAAATTTCAG AAAAACTGT AGAAGAAGTT CCAGTAAATC CAAATGAAGG 1320
 CACAGTAGAA GGTACCTCAA ATCAAGAAAC AGAAAAACCA GTTCAACCTG CAGAAGAAAC 1380
 ACAAACAAAC TCTGGGAAAA TAGCTAACGA AAATACTGGA GAAGTATCCA ATAAACCTAG 1440
 TGATTCAAAA CCACCAGTTG AAGAATCAAA TCAACCAGAA AAAACGGAA CTGCAACAAA 1500
 ACCAGAAAAT TCAGGTAATA CAACATCAGA GAATGGACAA ACAGAACCAG AACCATCAAA 1560
 CGGAAATTCA ACTGAGGATG TTTCAACCGA ATCAAACACA TCCAATTCAA ATGGAAACGA 1620
 AGAAATTAAA, CAAGAAAATG AACTAGACCC TGATAAAAAG GTAGAAGAAC CAGAGAAAAC 1680
 ACTTGAATTA AGAAATGTTT CCGACCTAGA GTTA 1714

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 571 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asn Tyr Asn Thr Asp Tyr Glu Leu Thr Ser Gly Glu Lys Leu Pro Leu
 1 5 10 15
 Pro Lys Glu Ile Ser Gly Tyr Thr Tyr Ile Gly Tyr Ile Lys Glu Gly
 20 25 30
 Lys Thr Thr Ser Glu Ser Glu Val Ser Asn Gln Lys Ser Ser Val Ala
 35 40 45
 Thr Pro Thr Lys Gln Gln Lys Val Asp Tyr Asn Val Thr Pro Asn Phe
 50 55 60
 Val Asp His Pro Ser Thr Val Gln Ala Ile Gln Glu Gln Thr Pro Val
 65 70 75 80
 Ser Ser Thr Lys Pro Thr Glu Val Gln Val Val Glu Lys Pro Phe Ser
 85 90 95
 Thr Glu Leu Ile Asn Pro Arg Lys Glu Glu Lys Gln Ser Ser Asp Ser
 100 105 110
 Gln Glu Gln Leu Ala Glu His Lys Asn Leu Glu Thr Lys Lys Glu Glu
 115 120 125
 Lys Ile Ser Pro Lys Glu Lys Thr Gly Val Asn Thr Leu Asn Pro Gln
 130 135 140
 Asp Glu Val Leu Ser Gly Gln Leu Asn Lys Pro Glu Leu Leu Tyr Arg
 145 150 155 160
 Glu Glu Thr Met Glu Thr Lys Ile Asp Phe Gln Glu Glu Ile Gln Glu
 165 170 175
 Asn Pro Asp Leu Ala Glu Gly Thr Val Arg Val Lys Gln Glu Gly Lys
 180 185 190
 Leu Gly Lys Lys Val Glu Ile Val Arg Ile Phe Ser Val Asn Lys Glu
 195 200 205
 Glu Val Ser Arg Glu Ile Val Ser Thr Ser Thr Thr Ala Pro Ser Pro
 210 215 220
 Arg Ile Val Glu Lys Gly Thr Lys Lys Thr Gln Val Ile Lys Glu Gln
 225 230 235 240
 Pro Glu Thr Gly Val Glu His Lys Asp Val Gln Ser Gly Ala Ile Val
 245 250 255
 Glu Pro Ala Ile Gln Pro Glu Leu Pro Glu Ala Val Val Ser Asp Lys

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cont.

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 748 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGAGAATCAA GCTACACCCA AAGAGACTAG CGCTCAAAAG ACAATCGTCC TTGCTACAGC 60
 TGGCGACGTG CCACCATTTG ACTACGAAGA CAAGGGCAAT CTGACAGGCT TTGATATCGA 120
 AGTTTTTAAAG GCAGTAGATG AAAAAGCTCAG CGACTACGAG ATTCAATTCC AAAGAACCGC 180
 CTGGGAGAGC ATCTTCCCAG GACTTGATTC TGGTCACTAT CAGGCTGCGG CCAATAACTT 240
 GAGTTACACA AAAGAGCGTG CTGAAAAATA CCTTTACTCG CTTCCAATTT CCAACAATCC 300
 CCTCGTCCTT GTCAGCAACA AGAAAAATCC TTTGACTTCT CTTGACCAGA TCGCTGGTAA 360
 AACAAACAAA GAGGATACCG GAACTTCTAA CGCTCAATTC ATCAATAACT GGAATCAGAA 420
 ACACACTGAT AATCCCGCTA CAATTAATTT TTCTGGTGAG GATATTGGTA AACGAATCCT 480
 AGACCTTGCT AACGGAGAGT TTGATTTCTT AGTTTTTGAC AAGGTATCCG TTCAAAAGAT 540
 TATCAAGGAC CGTGGTTTAG ACCTCTCAGT CGTTGATTTA CCTTCTGCAG ATAGCCCCAG 600
 CAATTATATC ATTTTCTCAA GCGACCAAAA AGAGTTTAAA GAGCAATTTG ATAAAGCGCT 660
 CAAAGAACTC TATCAAGACG GAACCCCTGA AAAAGCTCAGC AATACCTATC TAGGTGGTTC 720
 TTACCTCCCA GATCAATCTC AGTTACAA 748

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 249 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Asn Gln Ala Thr Pro Lys Glu Thr Ser Ala Gln Lys Thr Ile Val
 1 5 10 15
 Leu Ala Thr Ala Gly Asp Val Pro Pro Phe Asp Tyr Glu Asp Lys Gly
 20 25 30
 Asn Leu Thr Gly Phe Asp Ile Glu Val Leu Lys Ala Val Asp Glu Lys
 35 40 45
 Leu Ser Asp Tyr Glu Ile Gln Phe Gln Arg Thr Ala Trp Glu Ser Ile
 50 55 60
 Phe Pro Gly Leu Asp Ser Gly His Tyr Gln Ala Ala Asn Asn Leu
 65 70 75 80

Ser Tyr Thr Lys Glu Arg Ala Glu Lys Tyr Leu Tyr Ser Leu Pro Ile
 85 90 95
 Ser Asn Asn Pro Leu Val Leu Val Ser Asn Lys Lys Asn Pro Leu Thr
 100 105 110
 Ser Leu Asp Gln Ile Ala Gly Lys Thr Thr Gln Glu Asp Thr Gly Thr
 115 120 125
 Ser Asn Ala Gln Phe Ile Asn Asn Trp Asn Gln Lys His Thr Asp Asn
 130 135 140
 Pro Ala Thr Ile Asn Phe Ser Gly Glu Asp Ile Gly Lys Arg Ile Leu
 145 150 155 160
 Asp Leu Ala Asn Gly Glu Phe Asp Phe Leu Val Phe Asp Lys Val Ser
 165 170 175
 Val Gln Lys Ile Ile Lys Asp Arg Gly Leu Asp Leu Ser Val Val Asp
 180 185 190
 Leu Pro Ser Ala Asp Ser Pro Ser Asn Tyr Ile Ile Phe Ser Ser Asp
 195 200 205
 Gln Lys Glu Phe Lys Glu Gln Phe Asp Lys Ala Leu Lys Glu Leu Tyr
 210 215 220
 Gln Asp Gly Thr Leu Glu Lys Leu Ser Asn Thr Tyr Leu Gly Gly Ser
 225 230 235 240
 Tyr Leu Pro Asp Gln Ser Gln Leu Gln
 245

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 985 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TGGTAACCGC TCCTCTCGTA ACGCAGCTTC ATCTTCTGAT GTGAAGACAA AAGCAGCAAT	60
CGTCACTGAT ACTGGTGGTG TTGATGACAA ATCATTCAAC CAATCAGCTT GGAAGGTTT	120
GCAGGCTTGG GGTAAAGAAC ACAATCTTTC AAAAGATAAC GGTTCCTACTT ACTTCCAATC	180
AACAAGTGAA GCTGACTACG CTAACAACCTT GCAACAAGCG GCTGGAAGTT ACAACCTAAT	240
CTTCGGTGTT GGTTTTGCCC TTAATAATGC AGTTAAAGAT GCAGCAAAAG AACACACTGA	300
CTTGAACTAT GTCTTGATTG ATGATGTGAT TAAAGACCAA AAGAATGTTG CGAGCGTAAC	360
TTTCGCTGAT AATGAGTCAG GTTACCTTGC AGGTGTGGCT GCAGCAAAAA CAACTAAGAC	420
AAAACAAGTT GGTTTTGTAG GTGGTATCGA ATCTGAAGTT ATCTCTCGTT TTGAAGCAGG	480
ATTCAAGGCT GGTGTTGCGT CAGTAGACCC ATCTATCAAA GTCCAAGTTG ACTACGCTGG	540

TTCATTTGGT GATGCGGCTA AAGGTAAAAC AATTGCAGCC GCACAATACG CAGCCGGTGC 600
 AGATATTGTT TACCAAGTAG CTGGTGGTAC AGGTGCAGGT GTCTTTGCAG AGGCAAAATC 660
 TCTCAACGAA AGCCGTCCTG AAAATGAAAA AGTTTGGGTT ATCGGTGTTG ATCGTGACCA 720
 AGAAGCAGAA GGTAATACA CTCTAAAGA TGGCAAAGAA TCAAACTTTG TTCTTGATC 780
 TACTTTGAAA CAAGTTGGTA CAACTGTAAA AGATATTTCT AACAAAGCAG AAAGAGGAGA 840
 ATTCCCTGGC GGTCAAGTGA TCGTTTACTC ATTGAAGGAT AAAGGGGTG ACTTGGCAGT 900
 AACAAACCTT TCAGAAGAAG GTAAAAAAGC TGTCAAGAT GCAAAAGCTA AAATCCTTGA 960
 TGAAGCGTA AAAGTCCTG AAAAA 985

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Asn Arg Ser Ser Arg Asn Ala Ala Ser Ser Ser Asp Val Lys Thr
 1 5 10 15
 Lys Ala Ala Ile Val Thr Asp Thr Gly Gly Val Asp Asp Lys Ser Phe
 20 25 30
 Asn Gln Ser Ala Trp Glu Gly Leu Gln Ala Trp Gly Lys Glu His Asn
 35 40 45
 Leu Ser Lys Asp Asn Gly Phe Thr Tyr Phe Gln Ser Thr Ser Glu Ala
 50 55 60
 Asp Tyr Ala Asn Asn Leu Gln Gln Ala Ala Gly Ser Tyr Asn Leu Ile
 65 70 75 80
 Phe Gly Val Gly Phe Ala Leu Asn Asn Ala Val Lys Asp Ala Ala Lys
 85 90 95
 Glu His Thr Asp Leu Asn Tyr Val Leu Ile Asp Asp Val Ile Lys Asp
 100 105 110
 Gln Lys Asn Val Ala Ser Val Thr Phe Ala Asp Asn Glu Ser Gly Tyr
 115 120 125
 Leu Ala Gly Val Ala Ala Ala Lys Thr Thr Lys Thr Lys Gln Val Gly
 130 135 140
 Phe Val Gly Gly Ile Glu Ser Glu Val Ile Ser Arg Phe Glu Ala Gly
 145 150 155 160
 Phe Lys Ala Gly Val Ala Ser Val Asp Pro Ser Ile Lys Val Gln Val

165 170 175

Asp Tyr Ala Gly Ser Phe Gly Asp Ala Ala Lys Gly Lys Thr Ile Ala
180 185 190

Ala Ala Gln Tyr Ala Ala Gly Ala Asp Ile Val Tyr Gln Val Ala Gly
195 200 205

Gly Thr Gly Ala Gly Val Phe Ala Glu Ala Lys Ser Leu Asn Glu Ser
210 215 220

Arg Pro Glu Asn Glu Lys Val Trp Val Ile Gly Val Asp Arg Asp Gln
225 230 235 240

Glu Ala Glu Gly Lys Tyr Thr Ser Lys Asp Gly Lys Glu Ser Asn Phe
245 250 255

Val Leu Val Ser Thr Leu Lys Gln Val Gly Thr Thr Val Lys Asp Ile
260 265 270

Ser Asn Lys Ala Glu Arg Gly Glu Phe Pro Gly Gly Gln Val Ile Val
275 280 285

Tyr Ser Leu Lys Asp Lys Gly Val Asp Leu Ala Val Thr Asn Leu Ser
290 295 300

Glu Glu Gly Lys Lys Ala Val Glu Asp Ala Lys Ala Lys Ile Leu Asp
305 310 315 320

Gly Ser Val Lys Val Pro Glu Lys
325

a' cont.
(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1404 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGTGGAAATT TGACAGGTAA CAGCAAAAAA GCTGCTGATT CAGGTGACAA ACCTGTTATC	60
AAAATGTACC AAATCGGTGA CAAACCAGAC AACTTGGATG AATTGTTAGC AAATGCCAAC	120
AAAATCATTG AAGAAAAAGT TGGTGCCAAA TTGGATATCC AATACCTTGG CTGGGGTGAC	180
TATGGTAAGA AAATGTCAGT TATCACATCA TCTGGTGAAA ACTATGATAT TGCCTTTGCA	240
GATAACTATA TTGTAAATGC TCAAAAAGGT GCTTACGCTG ACTTGACAGA ATTGTACAAA	300
AAAGAAGGTA AAGACCTTTA CAAAGCACTT GACCCAGCTT ACATCAAGGG TAATACTGTA	360
AATGGTAAGA TTTACGCTGT TCCAGTTGCA GCCAACGTTG CATCATCTCA AAACCTTTGCC	420
TTCAACGGAA CTCTCCTTGC TAAATATGGT ATCGATATTT CAGGTGTTAC TTCTTACGAA	480
ACTCTTGAGC CAGTCTTGAA ACAAATCAAA GAAAAAGCTC CAGACGTAGT ACCATTTGCT	540
ATTGGTAAAG TTTTCATCCC ATCTGATAAT TTTGACTACC CAGTAGCAAA CGGTCTTCCA	600

TTCGTTATCG ACCTGAAGG CGATACTACT AAAGTTGTAA ACCGTTACGA AGTGCCTCGT 660
 TTCAAAGAAC ACTTGAAGAC TCTTCACAAA TTCTATGAAG CTGGCTACAT TCCAAAAGAC 720
 GTCGCAACAA GCGATACTTC CTTTGACCTT CAACAAGATA CTTGGTTCGT TCGTGAAGAA 780
 ACAGTAGGAC CAGCTGACTA CGGTAACAGC TTGCTTTCAC GTGTTGCCAA CAAAGATATC 840
 CAAATCAAAC CAATTACTAA CTTTCATCAAG NAAAACCAAA CAACACAAGT TGCTAACTTT 900
 GTCATCTCAA ACAACTCTAA GAACAAAGAA AAATCAATGG AAATCTTGAA CCTCTTGAAT 960
 ACGAACCCAG AACTCTTGAA CGGTCTTGTT TACGGTCCAG AAGGCAAGAA CTGGGAAAAA 1020
 ATTGAAGGTA AAGAAAACCG TGTTCGCGTT CTTGATGGCT ACAAAGGAAA CACTCACATG 1080
 GGTGGATGGA AACTGGTAA CAACTGGATC CTTTACATCA ACGAAAACGT TACAGACCAA 1140
 CAAATCGAAA ATTCTAAGAA AGAATTGGCA GAAGCTAAAG AATCTCCAGC GCTTGGATTT 1200
 ATCTTCAATA CTGACAATGT GAAATCTGAA ATCTCAGCTA TTGCTAACAC AATGCAACAA 1260
 TTTGATACAG CTATCAACAC TGGTACTGTA GACCCAGATA AAGCGATTCC AGAATTGATG 1320
 GAAAAATTGA AATCTGAAGG TGCCTACGAA AAAGTATTGA ACGAAATGCA AAAACAATAC 1380
 GATGAATTCT TGAAAAACAA AAAA 1404

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Gly Asn Leu Thr Gly Asn Ser Lys Lys Ala Ala Asp Ser Gly Asp
 1 5 10 15
 Lys Pro Val Ile Lys Met Tyr Gln Ile Gly Asp Lys Pro Asp Asn Leu
 20 25 30
 Asp Glu Leu Leu Ala Asn Ala Asn Lys Ile Ile Glu Glu Lys Val Gly
 35 40 45
 Ala Lys Leu Asp Ile Gln Tyr Leu Gly Trp Gly Asp Tyr Gly Lys Lys
 50 55 60
 Met Ser Val Ile Thr Ser Ser Gly Glu Asn Tyr Asp Ile Ala Phe Ala
 65 70 75 80
 Asp Asn Tyr Ile Val Asn Ala Gln Lys Gly Ala Tyr Ala Asp Leu Thr
 85 90 95
 Glu Leu Tyr Lys Lys Glu Gly Lys Asp Leu Tyr Lys Ala Leu Asp Pro

100 105 110
 Ala Tyr Ile Lys Gly Asn Thr Val Asn Gly Lys Ile Tyr Ala Val Pro
 115 120 125
 Val Ala Ala Asn Val Ala Ser Ser Gln Asn Phe Ala Phe Asn Gly Thr
 130 135 140
 Leu Leu Ala Lys Tyr Gly Ile Asp Ile Ser Gly Val Thr Ser Tyr Glu
 145 150 155 160
 Thr Leu Glu Pro Val Leu Lys Gln Ile Lys Glu Lys Ala Pro Asp Val
 165 170 175
 Val Pro Phe Ala Ile Gly Lys Val Phe Ile Pro Ser Asp Asn Phe Asp
 180 185 190
 Tyr Pro Val Ala Asn Gly Leu Pro Phe Val Ile Asp Leu Glu Gly Asp
 195 200 205
 Thr Thr Lys Val Val Asn Arg Tyr Glu Val Pro Arg Phe Lys Glu His
 210 215 220
 Leu Lys Thr Leu His Lys Phe Tyr Glu Ala Gly Tyr Ile Pro Lys Asp
 225 230 235 240
 Val Ala Thr Ser Asp Thr Ser Phe Asp Leu Gln Gln Asp Thr Trp Phe
 245 250 255
 Val Arg Glu Glu Thr Val Gly Pro Ala Asp Tyr Gly Asn Ser Leu Leu
 260 265 270
 Ser Arg Val Ala Asn Lys Asp Ile Gln Ile Lys Pro Ile Thr Asn Phe
 275 280 285
 Ile Lys Xaa Asn Gln Thr Thr Gln Val Ala Asn Phe Val Ile Ser Asn
 290 295 300
 Asn Ser Lys Asn Lys Glu Lys Ser Met Glu Ile Leu Asn Leu Leu Asn
 305 310 315 320
 Thr Asn Pro Glu Leu Leu Asn Gly Leu Val Tyr Gly Pro Glu Gly Lys
 325 330 335
 Asn Trp Glu Lys Ile Glu Gly Lys Glu Asn Arg Val Arg Val Leu Asp
 340 345 350
 Gly Tyr Lys Gly Asn Thr His Met Gly Gly Trp Asn Thr Gly Asn Asn
 355 360 365
 Trp Ile Leu Tyr Ile Asn Glu Asn Val Thr Asp Gln Gln Ile Glu Asn
 370 375 380
 Ser Lys Lys Glu Leu Ala Glu Ala Lys Glu Ser Pro Ala Leu Gly Phe
 385 390 395 400
 Ile Phe Asn Thr Asp Asn Val Lys Ser Glu Ile Ser Ala Ile Ala Asn
 405 410 415
 Thr Met Gln Gln Phe Asp Thr Ala Ile Asn Thr Gly Thr Val Asp Pro
 420 425 430
 Asp Lys Ala Ile Pro Glu Leu Met Glu Lys Leu Lys Ser Glu Gly Ala

435 440 445

Tyr Glu Lys Val Leu Asn Glu Met Gln Lys Gln Tyr Asp Glu Phe Leu
 450 455 460

Lys Asn Lys Lys
 465

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TGGTCAAGGA ACTGCTTCTA AAGACAACAA AGAGGCAGAA CTTAAGAAGG TTGACTTTTAT 60
 CCTAGACTGG ACACCAAATA CCAACCACAC AGGGCTTTAT GTTGCCAAGG AAAAAGGTTA 120
 TTTCAAAGAA GCTGGAGTGG ATGTTGATTT GAAATTGCCA CCAGAAGAAA GTTCTTCTGA 180
 CTTGGTTATC AACGGAAAGG CACCATTTCG AGTGATTTTC CAAGACTACA TGGCTAAGAA 240
 ATTGGAAGAAA GGAGCAGGAA TCACTGCCGT TGCAGCTATT GTTGAACACA ATACATCAGG 300
 AATCATCTCT CGTAAATCTG ATAATGTAAG CAGTCCAAAA GACTTGGTTG GTAAGAAATA 360
 TGGGACATGG AATGACCCAA CTGAACCTGC TATGTTGAAA ACCTTGGTAG AATCTCAAGG 420
 TGGAGACTTT GAGAAGGTTG AAAAAGTACC AAATAACGAC TCAAACCAA TCACACCGAT 480
 TGCCAATGGC GTCTTTGATA CTGCTTGGAT TTACTACGGT TGGGATGGTA TCCTTGCTAA 540
 ATCTCAAGGT GTAGATGCTA ACTTCATGTA CTTGAAAGAC TATGTCAAGG AGTTTGACTA 600
 CTATTCACCA GTTATCATCG CAAACAACGA CTATCTGAAA GATAACAAAG AAGAAGCTCG 660
 CAAAGTCATC CAAGCCATCA AAAAAGGCTA CCAATATGCC ATGGAACATC CAGAAGAAGC 720
 TGCAGATATT CTCATCAAGA ATGCACCTGA ACTCAAGGAA AAACGTGACT TTGTCATCGA 780
 ATCTCAAAAA TACTTGTCAA AAGAATACGC AAGCGACAAG GAAAAATGGG GTCAATTTGA 840
 CGCAGCTCGC TGGAAATGCTT TCTACAAATG GGATAAAGAA AATGGTATCC TTAAAGAAGA 900
 CTTGACAGAC AAAGGCTTCA CCAACGAATT TGTGAAA 937

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Gln Gly Thr Ala Ser Lys Asp Asn Lys Glu Ala Glu Leu Lys Lys
 1 5 10 15
 Val Asp Phe Ile Leu Asp Trp Thr Pro Asn Thr Asn His Thr Gly Leu
 20 25 30
 Tyr Val Ala Lys Glu Lys Gly Tyr Phe Lys Glu Ala Gly Val Asp Val
 35 40 45
 Asp Leu Lys Leu Pro Pro Glu Glu Ser Ser Ser Asp Leu Val Ile Asn
 50 55 60
 Gly Lys Ala Pro Phe Ala Val Tyr Phe Gln Asp Tyr Met Ala Lys Lys
 65 70 75 80
 Leu Glu Lys Gly Ala Gly Ile Thr Ala Val Ala Ala Ile Val Glu His
 85 90 95
 Asn Thr Ser Gly Ile Ile Ser Arg Lys Ser Asp Asn Val Ser Ser Pro
 100 105 110
 Lys Asp Leu Val Gly Lys Lys Tyr Gly Thr Trp Asn Asp Pro Thr Glu
 115 120 125
 Leu Ala Met Leu Lys Thr Leu Val Glu Ser Gln Gly Gly Asp Phe Glu
 130 135 140
 Lys Val Glu Lys Val Pro Asn Asn Asp Ser Asn Ser Ile Thr Pro Ile
 145 150 155 160
 Ala Asn Gly Val Phe Asp Thr Ala Trp Ile Tyr Tyr Gly Trp Asp Gly
 165 170 175
 Ile Leu Ala Lys Ser Gln Gly Val Asp Ala Asn Phe Met Tyr Leu Lys
 180 185 190
 Asp Tyr Val Lys Glu Phe Asp Tyr Tyr Ser Pro Val Ile Ile Ala Asn
 195 200 205
 Asn Asp Tyr Leu Lys Asp Asn Lys Glu Glu Ala Arg Lys Val Ile Gln
 210 215 220
 Ala Ile Lys Lys Gly Tyr Gln Tyr Ala Met Glu His Pro Glu Glu Ala
 225 230 235 240
 Ala Asp Ile Leu Ile Lys Asn Ala Pro Glu Leu Lys Glu Lys Arg Asp
 245 250 255
 Phe Val Ile Glu Ser Gln Lys Tyr Leu Ser Lys Glu Tyr Ala Ser Asp
 260 265 270
 Lys Glu Lys Trp Gly Gln Phe Asp Ala Ala Arg Trp Asn Ala Phe Tyr
 275 280 285
 Lys Trp Asp Lys Glu Asn Gly Ile Leu Lys Glu Asp Leu Thr Asp Lys
 290 295 300
 Gly Phe Thr Asn Glu Phe Val Lys
 305 310

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TAGCTCAGGT GGAAACGCTG GTTCATCCTC TGGAAAAACA ACTGCCAAAG CTCGCACTAT 60
 CGATGAAATC AAAAAAAGCG GTGAAGTGGC AATCGCCGTG TTTGGAGATA AAAAACCGTT 120
 TGGCTACGTT GACAATGATG GTTCTACCAA GGTACGCTAC GATATTGAAC TAGGGAACCA 180
 ACTAGCTCAA GACCTTGGTG TCAAGGTTAA ATACATTTC A GTCGATGCTG CCAACCGTGC 240
 GGAATACTTG ATTTCAAACA AGGTAGATAT TACTCTTGCT AACTTTACAG TAACTGACGA 300
 ACGTAAGAAA CAAGTTGATT TTGCCCTTCC ATATATGAAA GTTTCTCTGG GTGTCGTATC 360
 ACCTAAGACT GGTCTCATTA CAGACGTCAA ACAACTTGAA GGTAAACCT TAATTGTCAC 420
 AAAAGGAACG ACTGCTGAGA CTTATTTTGA AAAGAATCAT CCAGAAATCA AACTCCAAAA 480
 ATACGACCAA TACAGTGAAT CTTACCAAGC TCTTCTTGAC GGACGTGGAG ATGCCTTTTC 540
 AACTGACAAT ACGGAAGTTC TAGCTTGGGC GCTTGAAAAT AAAGGATTTG AAGTAGGAAT 600
 TACTTCCCTC GGTGATCCCG ATACCATTGC GGCAGCAGTT CAAAAAGGCA ACCAAGAATT 660
 GCTAGACTTC ATCAATAAAG ATATTGAAAA ATTAGGCAAG GAAACTTCT TCCACAAGGC 720
 CTATGAAAAG ACACTTCACC CAACCTACGG TGACGCTGCT AAAGCAGATG ACCTGGTTGT 780
 TGAAGGTGGA AAAGTTGAT 799

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser Ser Gly Gly Asn Ala Gly Ser Ser Ser Gly Lys Thr Thr Ala Lys
 1 5 10 15
 Ala Arg Thr Ile Asp Glu Ile Lys Lys Ser Gly Glu Leu Arg Ile Ala
 20 25 30
 Val Phe Gly Asp Lys Lys Pro Phe Gly Tyr Val Asp Asn Asp Gly Ser

35 40 45
 Thr Lys Val Arg Tyr Asp Ile Glu Leu Gly Asn Gln Leu Ala Gln Asp
 50 55 60
 Leu Gly Val Lys Val Lys Tyr Ile Ser Val Asp Ala Ala Asn Arg Ala
 65 70 75 80
 Glu Tyr Leu Ile Ser Asn Lys Val Asp Ile Thr Leu Ala Asn Phe Thr
 85 90 95
 Val Thr Asp Glu Arg Lys Lys Gln Val Asp Phe Ala Leu Pro Tyr Met
 100 105 110
 Lys Val Ser Leu Gly Val Val Ser Pro Lys Thr Gly Leu Ile Thr Asp
 115 120 125
 Val Lys Gln Leu Glu Gly Lys Thr Leu Ile Val Thr Lys Gly Thr Thr
 130 135 140
 Ala Glu Thr Tyr Phe Glu Lys Asn His Pro Glu Ile Lys Leu Gln Lys
 145 150 155 160
 Tyr Asp Gln Tyr Ser Asp Ser Tyr Gln Ala Leu Leu Asp Gly Arg Gly
 165 170 175
 Asp Ala Phe Ser Thr Asp Asn Thr Glu Val Leu Ala Trp Ala Leu Glu
 180 185 190
 Asn Lys Gly Phe Glu Val Gly Ile Thr Ser Leu Gly Asp Pro Asp Thr
 195 200 205
 Ile Ala Ala Ala Val Gln Lys Gly Asn Gln Glu Leu Leu Asp Phe Ile
 210 215 220
 Asn Lys Asp Ile Glu Lys Leu Gly Lys Glu Asn Phe Phe His Lys Ala
 225 230 235 240
 Tyr Glu Lys Thr Leu His Pro Thr Tyr Gly Asp Ala Ala Lys Ala Asp
 245 250 255
 Asp Leu Val Val Glu Gly Gly Lys Val Asp
 260 265

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTCCAACATAT GGTAAATCTG CGGATGGCAC AGTGACCATC GAGTATTTCA ACCAGAAAAA 60
 AGAAATGACC AAAACCTTGG AAGAAATCAC TCGTGATTTT GAGAAGGAAA ACCCTAAGAT 120
 CAAGGTCAAA GTCGTCAATG TACCAAATGC TGGTGAAGTA TTGAAGACAC GCGTTCTCGC 180
 AGGAGATGTG CCTGATGTGG TCAATATTTA CCCACAGTCC ATCGAACTGC AAGAATGGGC 240

AAAAGCAGGT GTTTTTGAAG ATTTGAGCAA CAAAGACTAC CTGAAACGCG TGAAAAATGG 300
 CTACGCTGAA AAATATGCTG TAAACGAAAA AGTTTACAAC GTTCCTTTTA CAGCTAATGC 360
 TTATGGAATT TACTACAACA AAGATAAATT CGAAGAACTG GGCTTGAAGG TTCCTGAAAC 420
 CTGGGATGAA TTTGAACAGT TAGTCAAAGA TATCGTTGCT AAAGGACAAA CACCATTGG 480
 AATTGCAGGT GCAGATGCTT GGACACTCAA TGGTTACAAT CAATTAGCCT TTGCGACAGC 540
 AACAGGTGGA GGAAAAGAAG CAAATCAATA CCTTCGTTAT TCTCAACCAA ATGCCATTAA 600
 ATTGTCGGAT CCGATTATGA AAGATGATAT CAAGGTCATG GACATCCTTC GCATCAATGG 660
 ATCTAAGCAA AAGAACTGGG AAGGTGCTGG CTATACCGAT GTTATCGGAG CCTTCGCACG 720
 TGGGGATGTC CTCATGACAC CAAATGGGTC TTGGGCGATC ACAGCGATTA ATGAACAAAA 780
 ACCGAACTTT AAGATTGGGA CCTTCATGAT TCCAGGAAAA GAAAAAGGAC AAAGCTTAAC 840
 CGTTGGTGGC GGAGACTTGG CATGGTCTAT CTCAGCCACC ACCAAACATC CAAAAGAAGC 900
 CAATGCCCTTT GTGGAATATA TGACCCGTCC AGAAGTCATG CAAAATACT ACGATGTGGA 960
 CGGATCTCCA ACAGCGATCG AAGGGGTCAA ACAAGCAGGA GAAGATTAC CGCTTGCTGG 1020
 TATGACCGAA TATGCCTTTA CGGATCGTCA CTTGGTCTGG TTGCAACAAT ACTGGACCAG 1080
 TGAAGCAGAC TTCCATACCT TGACCATGAA CTATGTCTTG ACCGGTGATA AACAAGGCAT 1140
 GGTCAATGAT TTGAATGCCT TCTTTAACCC GATGAAAGCG GATGTGGAT 1189

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Asn Tyr Gly Lys Ser Ala Asp Gly Thr Val Thr Ile Glu Tyr Phe
 1 5 10 15
 Asn Gln Lys Lys Glu Met Thr Lys Thr Leu Glu Glu Ile Thr Arg Asp
 20 25 30
 Phe Glu Lys Glu Asn Pro Lys Ile Lys Val Lys Val Val Asn Val Pro
 35 40 45
 Asn Ala Gly Glu Val Leu Lys Thr Arg Val Leu Ala Gly Asp Val Pro
 50 55 60
 Asp Val Val Asn Ile Tyr Pro Gln Ser Ile Glu Leu Gln Glu Trp Ala
 65 70 75 80

Lys Ala Gly Val Phe Glu Asp Leu Ser Asn Lys Asp Tyr Leu Lys Arg
 85 90 95
 Val Lys Asn Gly Tyr Ala Glu Lys Tyr Ala Val Asn Glu Lys Val Tyr
 100 105 110
 Asn Val Pro Phe Thr Ala Asn Ala Tyr Gly Ile Tyr Tyr Asn Lys Asp
 115 120 125
 Lys Phe Glu Glu Leu Gly Leu Lys Val Pro Glu Thr Trp Asp Glu Phe
 130 135 140
 Glu Gln Leu Val Lys Asp Ile Val Ala Lys Gly Gln Thr Pro Phe Gly
 145 150 155 160
 Ile Ala Gly Ala Asp Ala Trp Thr Leu Asn Gly Tyr Asn Gln Leu Ala
 165 170 175
 Phe Ala Thr Ala Thr Gly Gly Gly Lys Glu Ala Asn Gln Tyr Leu Arg
 180 185 190
 Tyr Ser Gln Pro Asn Ala Ile Lys Leu Ser Asp Pro Ile Met Lys Asp
 195 200 205
 Asp Ile Lys Val Met Asp Ile Leu Arg Ile Asn Gly Ser Lys Gln Lys
 210 215 220
 Asn Trp Glu Gly Ala Gly Tyr Thr Asp Val Ile Gly Ala Phe Ala Arg
 225 230 235 240
 Gly Asp Val Leu Met Thr Pro Asn Gly Ser Trp Ala Ile Thr Ala Ile
 245 250 255
 Asn Glu Gln Lys Pro Asn Phe Lys Ile Gly Thr Phe Met Ile Pro Gly
 260 265 270
 Lys Glu Lys Gly Gln Ser Leu Thr Val Gly Ala Gly Asp Leu Ala Trp
 275 280 285
 Ser Ile Ser Ala Thr Thr Lys His Pro Lys Glu Ala Asn Ala Phe Val
 290 295 300
 Glu Tyr Met Thr Arg Pro Glu Val Met Gln Lys Tyr Tyr Asp Val Asp
 305 310 315 320
 Gly Ser Pro Thr Ala Ile Glu Gly Val Lys Gln Ala Gly Glu Asp Ser
 325 330 335
 Pro Leu Ala Gly Met Thr Glu Tyr Ala Phe Thr Asp Arg His Leu Val
 340 345 350
 Trp Leu Gln Gln Tyr Trp Thr Ser Glu Ala Asp Phe His Thr Leu Thr
 355 360 365
 Met Asn Tyr Val Leu Thr Gly Asp Lys Gln Gly Met Val Asn Asp Leu
 370 375 380
 Asn Ala Phe Phe Asn Pro Met Lys Ala Asp Val Asp
 385 390 395

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TGGGAAAAAT TCTAGCGAAA CTAGTGGAGA TAATTGGTCA AAGTACCAGT CTAACAAGTC 60
 TATTACTATT GGATTGATA GTACTTTTGT TCCAATGGGA TTGCTCAGA AAGATGGTTC 120
 TTATGCAGGA TTTGATATTG ATTTAGCTAC AGCTGTTTTT GAAAAATACG GAATCACGGT 180
 AAATTGGCAA CCGATTGATT GGGATTTGAA AGAAGCTGAA TTGACAAAAG GAACGATTGA 240
 TCTGATTTGG AATGGCTATT CCGCTACAGA CGAACGCCGT GAAAAGGTGG CTTTCAGTAA 300
 CTCATATATG AAGAATGAGC AGGTATTGGT TACGAAGAAA TCATCTGGTA TCACGACTGC 360
 AAAGGATATG ACTGGAAAGA CATTAGGAGC TCAAGCTGGT TCATCTGGTT ATGCGGACTT 420
 TGAAGCAAAT CCAGAAATTT TGAAGAATAT TGTCGCTAAT AAGGAAGCGA ATCAATACCA 480
 AACCTTTAAT GAAGCCTTGA TTGATTTGAA AAACGATCGA ATTGATGGTC TATTGATTGA 540
 CCGTGTCTAT GCAAACATTT ATTTAGAAGC AGAAGGTGTT TTAAACGATT ATAATGTCCT 600
 TACAGTTGGA CTAGAAACAG AAGCTTTTGC GGTGAGGCC CGTAAGGAAG ATACAAACTT 660
 GGTTAAGAAG ATAAATGAAG CTTTTTCTAG TCTTTACAAG GACGGCAAGT TCCAAGAAAT 720
 CAGCCAAAAA TGGTTTGGAG AAGATGTAGC AACCAAAGAA GTAAAAGAAG GACAG 775

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly Lys Asn Ser Ser Glu Thr Ser Gly Asp Asn Trp Ser Lys Tyr Gln
 1 5 10 15
 Ser Asn Lys Ser Ile Thr Ile Gly Phe Asp Ser Thr Phe Val Pro Met
 20 25 30
 Gly Phe Ala Gln Lys Asp Gly Ser Tyr Ala Gly Phe Asp Ile Asp Leu
 35 40 45
 Ala Thr Ala Val Phe Glu Lys Tyr Gly Ile Thr Val Asn Trp Gln Pro
 50 55 60
 Ile Asp Trp Asp Leu Lys Glu Ala Glu Leu Thr Lys Gly Thr Ile Asp

65 70 75 80

Leu Ile Trp Asn Gly Tyr Ser Ala Thr Asp Glu Arg Arg Glu Lys Val
85 90 95

Ala Phe Ser Asn Ser Tyr Met Lys Asn Glu Gln Val Leu Val Thr Lys
100 105 110

Lys Ser Ser Gly Ile Thr Thr Ala Lys Asp Met Thr Gly Lys Thr Leu
115 120 125

Gly Ala Gln Ala Gly Ser Ser Gly Tyr Ala Asp Phe Glu Ala Asn Pro
130 135 140

Glu Ile Leu Lys Asn Ile Val Ala Asn Lys Glu Ala Asn Gln Tyr Gln
145 150 155 160

Thr Phe Asn Glu Ala Leu Ile Asp Leu Lys Asn Asp Arg Ile Asp Gly
165 170 175

Leu Leu Ile Asp Arg Val Tyr Ala Asn Tyr Tyr Leu Glu Ala Glu Gly
180 185 190

Val Leu Asn Asp Tyr Asn Val Phe Thr Val Gly Leu Glu Thr Glu Ala
195 200 205

Phe Ala Val Gly Ala Arg Lys Glu Asp Thr Asn Leu Val Lys Lys Ile
210 215 220

Asn Glu Ala Phe Ser Ser Leu Tyr Lys Asp Gly Lys Phe Gln Glu Ile
225 230 235 240

Ser Gln Lys Trp Phe Gly Glu Asp Val Ala Thr Lys Glu Val Lys Glu
245 250 255

Gly Gln

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 868 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGCTAGCGGA AAAAAAGATA CAACTTCTGG TCAAAACTA AAAGTTGTTG CTACAAACTC	60
AATCATCGCT GATATTACTA AAAATATTGC TGGTGACAAA ATTGACCTTC ATAGTATCGT	120
TCCGATTGGG CAAGACCCAC ACGAATACGA ACCACTTCCT GAAGACGTTA AGAAACTTTC	180
TGAGGCTAAT TTGATTTTCT ATAACGGTAT CAACCTTGAA ACAGGTGGCA ATGCTTGGTT	240
TACAAAATTG GTAGAAAATG CCAAGAAAAC TGAAAACAAA GACTACTTCG CAGTCAGCGA	300
CGGCGTTGAT GTTATCTACC TTGAAGGTCA AAATGAAAAA GGAAAAGAAG ACCCACACGC	360
TTGGCTTAAC CTTGAAAACG GTATTATTTT TGCTAAAAAT ATCGCCAAAC AATTGAGCGC	420

CAAAGACCTT AACAAATAAG AATTCTATGA AAAAAATCTC AAAGAATATA CTGATAAGTT 480
AGACAAACTT GATAAAGAAA GTAAGGATAA ATTTAATAAG ATCCCTGCTG AAAAGAAACT 540
CATTGTAACC AGCGAAGGAG CATTCAAATA CTTCTCTAAA GCCTATGGTG TCCCAAGTGC 600
TTACATCTGG GAAATCAATA CTGAAGAAGA AGGAACTCCT GAACAAATCA AGACCTTGGT 660
TGAAAAACTT CGCCAAACAA AAGTTCCATC ACTCTTTGTA GAATCAAGTG TGGATGACCG 720
TCCAATGAAA ACTGTTTCTC AAGACACAAA CATCCCAATC TACGCTCAAA TCTTTACTGA 780
CTCTATCGCA GAACAAGGTA AAGAAGGCGA CAGCTACTAC AGCATGATGA AATACAACCT 840
TGACAAGATT GCTGAAGGAT TGGCAAAA 868

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala Ser Gly Lys Lys Asp Thr Thr Ser Gly Gln Lys Leu Lys Val Val
1 5 10 15
Ala Thr Asn Ser Ile Ile Ala Asp Ile Thr Lys Asn Ile Ala Gly Asp
20 25 30
Lys Ile Asp Leu His Ser Ile Val Pro Ile Gly Gln Asp Pro His Glu
35 40 45
Tyr Glu Pro Leu Pro Glu Asp Val Lys Lys Thr Ser Glu Ala Asn Leu
50 55 60
Ile Phe Tyr Asn Gly Ile Asn Leu Glu Thr Gly Gly Asn Ala Trp Phe
65 70 75 80
Thr Lys Leu Val Glu Asn Ala Lys Lys Thr Glu Asn Lys Asp Tyr Phe
85 90 95
Ala Val Ser Asp Gly Val Asp Val Ile Tyr Leu Glu Gly Gln Asn Glu
100 105 110
Lys Gly Lys Glu Asp Pro His Ala Trp Leu Asn Leu Glu Asn Gly Ile
115 120 125
Ile Phe Ala Lys Asn Ile Ala Lys Gln Leu Ser Ala Lys Asp Pro Asn
130 135 140
Asn Lys Glu Phe Tyr Glu Lys Asn Leu Lys Glu Tyr Thr Asp Lys Leu
145 150 155 160
Asp Lys Leu Asp Lys Glu Ser Lys Asp Lys Phe Asn Lys Ile Pro Ala

165	170	175
Glu Lys Lys Leu Ile Val Thr Ser	Glu Gly Ala Phe Lys Tyr Phe Ser	
180	185	190
Lys Ala Tyr Gly Val Pro Ser Ala Tyr Ile Trp Glu Ile Asn Thr Glu		
195	200	205
Glu Glu Gly Thr Pro Glu Gln Ile Lys Thr Leu Val Glu Lys Leu Arg		
210	215	220
Gln Thr Lys Val Pro Ser Leu Phe Val Glu Ser Ser Val Asp Asp Arg		
225	230	235
Pro Met Lys Thr Val Ser Gln Asp Thr Asn Ile Pro Ile Tyr Ala Gln		
245	250	255
Ile Phe Thr Asp Ser Ile Ala Glu Gln Gly Lys Glu Gly Asp Ser Tyr		
260	265	270
Tyr Ser Met Met Lys Tyr Asn Leu Asp Lys Ile Ala Glu Gly Leu Ala		
275	280	285
Lys		

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1546 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TGGCTCAAAA AATACAGCTT CAAGTCCAGA TTATAAGTTG GAAGGTGTAA CATTCCCGCT 60

TCAAGAAAAG AAAACATTGA AGTTTATGAC AGCCAGTTCA CCGTTATCTC CTAAAGACCC 120

AAATGAAAAG TTAATTTTGC AACGTTTGGA GAAGGAACT GGCCTTCATA TTGACTGGAC 180

CAACTACCAA TCCGACTTTG CAGAAAAACG TAACTTGGAT ATTTCTAGTG GTGATTTACC 240

AGATGCTATC CACAACGACG GAGCTTCAGA TGTGGACTTG ATGAACTGGG CTAAAAAAGG 300

TGTTATTATT CCAGTTGAAG ATTTGATTGA TAAATACATG CCAAATCTTA AGAAAAATTT 360

GGATGAGAAA CCAGAGTACA AGGCCTTGAT GACAGCACCT GATGGGCACA TTTACTCATT 420

TCCATGGATT GAAGAGCTTG GAGATGGTAA AGAGTCTATT CACAGTGTCA ACGATATGGC 480

TTGGATTAAAC AAAGATTGGC TTAAGAACT TGGTCTTGAA ATGCCAAAAA CTA CTGATGA 540

TTTGATTAAA GTCCTAGAAG CTTTCAAAAA CGGGGATCCA AATGGAAATG GAGAGGCTGA 600

TGAAATCCA TTTTCATTTA TTAGTGGTAA CGGAAACGAA GATTTTAAAT TCCTATTTGC 660

TGCATTTGGT ATAGGGGATA ACGATGATCA TTTAGTAGTA GGAAATGATG GCAAAGTTGA 720

CTTCACAGCA GATAACGATA ACTATAAAGA AGGTGTCAAA TTTATCCGTC AATTGCAAGA 780

AAAAGGCCTG ATTGATAAAG AAGCTTTTCGA ACATGATTGG AATAGTTACA TTGCTAAAGG 840
 TCATGATCAG AAATTTGGTG TTTACTTTAC ATGGGATAAG AATAATGTTA CTGGAAGTAA 900
 CGAAAGTTAT GATGTTTTAC CAGTACTTGC TGGACCAAGT GGTCAAAAAC ACGTAGCTCG 960
 TACAAACGGT ATGGGATTTG CACGTGACAA GATGGTTATT ACCAGTGTA AAAAAACCT 1020
 AGAATTGACA GCTAAATGGA TTGATGCACA ATACGCTCCA CTCCAATCTG TGCAAAATAA 1080
 CTGGGGAAC TACGGAGATG ACAAACAACA AAACATCTTT GAATTGGATC AAGCGTCAAA 1140
 TAGTCTAAAA CACTTACCAC TAAACGGAAC TGCACCAGCA GAACTTCGTC AAAAGACTGA 1200
 AGTAGGAGGA CCACTAGCTA TCCTAGATTC ATACTATGGT AAAGTAACAA CCATGCCTGA 1260
 TGATGCCAAA TGGCGTTTGG ATCTTATCAA AGAATATTAT GTTCCTTACA TGAGCAATGT 1320
 CAATAACTAT CCAAGAGTCT TTATGACACA GGAAGATTG GACAAGATTG CCCATATCGA 1380
 AGCAGATATG AATGACTATA TCTACCGTAA ACGTGCTGAA TGGATTGTAA ATGGCAATAT 1440
 TGATACTGAG TGGGATGATT ACAAGAAAGA ACTTGAAAAA TACGGACTTT CTGATTACCT 1500
 CGCTATTAAA CAAAATACT ACGACCAATA CCAAGCAAAC AAAAAC 1546

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 515 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gly Ser Lys Asn Thr Ala Ser Ser Pro Asp Tyr Lys Leu Glu Gly Val
 1 5 10 15
 Thr Phe Pro Leu Gln Glu Lys Lys Thr Leu Lys Phe Met Thr Ala Ser
 20 25 30
 Ser Pro Leu Ser Pro Lys Asp Pro Asn Glu Lys Leu Ile Leu Gln Arg
 35 40 45
 Leu Glu Lys Glu Thr Gly Val His Ile Asp Trp Thr Asn Tyr Gln Ser
 50 55 60
 Asp Phe Ala Glu Lys Arg Asn Leu Asp Ile Ser Ser Gly Asp Leu Pro
 65 70 75 80
 Asp Ala Ile His Asn Asp Gly Ala Ser Asp Val Asp Leu Met Asn Trp
 85 90 95
 Ala Lys Lys Gly Val Ile Ile Pro Val Glu Asp Leu Ile Asp Lys Tyr
 100 105 110

Met Pro Asn Leu Lys Lys Ile Leu Asp Glu Lys Pro Glu Tyr Lys Ala
 115 120 125
 Leu Met Thr Ala Pro Asp Gly His Ile Tyr Ser Phe Pro Trp Ile Glu
 130 135 140
 Glu Leu Gly Asp Gly Lys Glu Ser Ile His Ser Val Asn Asp Met Ala
 145 150 155 160
 Trp Ile Asn Lys Asp Trp Leu Lys Lys Leu Gly Leu Glu Met Pro Lys
 165 170 175
 Thr Thr Asp Asp Leu Ile Lys Val Leu Glu Ala Phe Lys Asn Gly Asp
 180 185 190
 Pro Asn Gly Asn Gly Glu Ala Asp Glu Ile Pro Phe Ser Phe Ile Ser
 195 200 205
 Gly Asn Gly Asn Glu Asp Phe Lys Phe Leu Phe Ala Ala Phe Gly Ile
 210 215 220
 Gly Asp Asn Asp Asp His Leu Val Val Gly Asn Asp Gly Lys Val Asp
 225 230 235 240
 Phe Thr Ala Asp Asn Asp Asn Tyr Lys Glu Gly Val Lys Phe Ile Arg
 245 250 255
 Gln Leu Gln Glu Lys Gly Leu Ile Asp Lys Glu Ala Phe Glu His Asp
 260 265 270
 Trp Asn Ser Tyr Ile Ala Lys Gly His Asp Gln Lys Phe Gly Val Tyr
 275 280 285
 Phe Thr Trp Asp Lys Asn Asn Val Thr Gly Ser Asn Glu Ser Tyr Asp
 290 295 300
 Val Leu Pro Val Leu Ala Gly Pro Ser Gly Gln Lys His Val Ala Arg
 305 310 315 320
 Thr Asn Gly Met Gly Phe Ala Arg Asp Lys Met Val Ile Thr Ser Val
 325 330 335
 Asn Lys Asn Leu Glu Leu Thr Ala Lys Trp Ile Asp Ala Gln Tyr Ala
 340 345 350
 Pro Leu Gln Ser Val Gln Asn Asn Trp Gly Thr Tyr Gly Asp Asp Lys
 355 360 365
 Gln Gln Asn Ile Phe Glu Leu Asp Gln Ala Ser Asn Ser Leu Lys His
 370 375 380
 Leu Pro Leu Asn Gly Thr Ala Pro Ala Glu Leu Arg Gln Lys Thr Glu
 385 390 395 400
 Val Gly Gly Pro Leu Ala Ile Leu Asp Ser Tyr Tyr Gly Lys Val Thr
 405 410 415
 Thr Met Pro Asp Asp Ala Lys Trp Arg Leu Asp Leu Ile Lys Glu Tyr
 420 425 430
 Tyr Val Pro Tyr Met Ser Asn Val Asn Asn Tyr Pro Arg Val Phe Met
 435 440 445

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cont.

Thr Gln Glu Asp Leu Asp Lys Ile Ala His Ile Glu Ala Asp Met Asn
 450 455 460

Asp Tyr Ile Tyr Arg Lys Arg Ala Glu Trp Ile Val Asn Gly Asn Ile
 465 470 475 480

Asp Thr Glu Trp Asp Asp Tyr Lys Lys Glu Leu Glu Lys Tyr Gly Leu
 485 490 495

Ser Asp Tyr Leu Ala Ile Lys Gln Lys Tyr Tyr Asp Gln Tyr Gln Ala
 500 505 510

Asn Lys Asn
 515

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 895 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TAGTACAAAC TCAAGCACTA GTCAGACAGA GACCAGTAGC TCTGCTCCAA CAGAGGTAAC 60
 CATTAAAAGT TCACTGGACG AGGTCAAAC TCCAAAGTT CCTGAAAAGA TTGTGACCTT 120
 TGACCTCGGC GCTGCGGATA CTATTCGCGC TTTAGGATTT GAAAAAATA TCGTCGGAAT 180
 GCCTACAAAA ACTGTTCCGA CTATCTAAA AGACCTAGTG GGAACGTCA AAAATGTTGG 240
 TTCTATGAAA GAACCTGATT TAGAAGCTAT CGCCGCCCTT GAGCCTGATT TGATTATCGC 300
 TTCGCCACGT ACACAAAAT TCGTAGACAA ATTCAAAGAA ATCGCCCCAA CCGTTCTCTT 360
 CCAAGCAAGC AAGGACGACT ACTGGACTTC TACCAAGGCT AATATCGAAT CCTTAGCAAG 420
 TGCCTTCGGC GAAACTGGTA CACAGAAAGC CAAGGAAGAA TTGACCAAGC TAGACAAGAG 480
 CATCCAAGAA GTCGCTACTA AAAATGAAAG CTCTGACAAA AAAGCCCTTG CGATCCTCCT 540
 TAATGAAGGA AAAATGGCAG CCTTTGGTGC CAAATCTCGT TTCTCTTTCT TGTACCAAAC 600
 CTTGAAATTC AAACCAACTG ATACAAAATT TGAAGACTCA CGCCACGGAC AAGAAGTCAG 660
 CTTTGAAAGT GTCAAAGAAA TCAACCCTGA CATCCTCTTT GTCATCAACC GTACCCTTGC 720
 CATCGGTGGG GACAACTCTA GCAACGACGG TGTCTAGAA AATGCCCTTA TCGCTGAAAC 780
 ACCTGCTGCT AAAAATGGTA AGATTATCCA ACTAACACCA GACCTCTGGT ATCTAAGCGG 840
 AGGCGGACTT GAATCAACAA AACTCATGAT TGAAGACATA CAAAAGCTT TGAAA 895

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Thr Asn Ser Ser Thr Ser Gln Thr Glu Thr Ser Ser Ser Ala Pro
 1 5 10 15
 Thr Glu Val Thr Ile Lys Ser Ser Leu Asp Glu Val Lys Leu Ser Lys
 20 25 30
 Val Pro Glu Lys Ile Val Thr Phe Asp Leu Gly Ala Ala Asp Thr Ile
 35 40 45
 Arg Ala Leu Gly Phe Glu Lys Asn Ile Val Gly Met Pro Thr Lys Thr
 50 55 60
 Val Pro Thr Tyr Leu Lys Asp Leu Val Gly Thr Val Lys Asn Val Gly
 65 70 75 80
 Ser Met Lys Glu Pro Asp Leu Glu Ala Ile Ala Ala Leu Glu Pro Asp
 85 90 95
 Leu Ile Ile Ala Ser Pro Arg Thr Gln Lys Phe Val Asp Lys Phe Lys
 100 105 110
 Glu Ile Ala Pro Thr Val Leu Phe Gln Ala Ser Lys Asp Asp Tyr Trp
 115 120 125
 Thr Ser Thr Lys Ala Asn Ile Glu Ser Leu Ala Ser Ala Phe Gly Glu
 130 135 140
 Thr Gly Thr Gln Lys Ala Lys Glu Glu Leu Thr Lys Leu Asp Lys Ser
 145 150 155 160
 Ile Gln Glu Val Ala Thr Lys Asn Glu Ser Ser Asp Lys Lys Ala Leu
 165 170 175
 Ala Ile Leu Leu Asn Glu Gly Lys Met Ala Ala Phe Gly Ala Lys Ser
 180 185 190
 Arg Phe Ser Phe Leu Tyr Gln Thr Leu Lys Phe Lys Pro Thr Asp Thr
 195 200 205
 Lys Phe Glu Asp Ser Arg His Gly Gln Glu Val Ser Phe Glu Ser Val
 210 215 220
 Lys Glu Ile Asn Pro Asp Ile Leu Phe Val Ile Asn Arg Thr Leu Ala
 225 230 235 240
 Ile Gly Gly Asp Asn Ser Ser Asn Asp Gly Val Leu Glu Asn Ala Leu
 245 250 255
 Ile Ala Glu Thr Pro Ala Ala Lys Asn Gly Lys Ile Ile Gln Leu Thr
 260 265 270
 Pro Asp Leu Trp Tyr Leu Ser Gly Gly Gly Leu Glu Ser Thr Lys Leu
 275 280 285

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 cont-

Met Ile Glu Asp Ile Gln Lys Ala Leu Lys
290 295

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TGGCAATTCT GGCGGAAGTA AAGATGCTGC CAAATCAGGT GGTGACGGTG CAAAAACAGA 60
 AATCACTTGG TGGGCATTCC CAGTATTTAC CCAAGAAAAA ACTGGTGACG GTGTTGGAAC 120
 TTATGAAAAA TCAATCATCG AAGCGTTTGA AAAAGCAAAC CCAGATATAA AAGTGAAATT 180
 GGAAACCATC GACTTCAAGT CAGGTCCTGA AAAATCACA ACAGCCATCG AAGCAGGAAC 240
 AGCTCCAGAC GTACTCTTTG ATGCACCAGG ACGTATCATC CAATACGGTA AAAACGGTAA 300
 ATTGGCTGAG TTGAATGACC TCTTCACAGA TGAATTTGTT AAAGATGTCA ACAATGAAAA 360
 CATCGTACAA GCAAGTAAAG CTGGAGACAA GGCTTATATG TATCCGATTA GTTCTGCCCC 420
 ATTCTACATG GCAATGAACA AGAAAATGTT AGAAGATGCT GGAGTAGCAA ACCTTGTAAG 480
 AGAAGGTTGG ACAACTGATG ATTTTGAAGA AGTATTGAAA GCACTTAAAG ACAAGGGTTA 540
 CACACCAGGT TCATTGTTCA GTTCTGGTCA AGGGGGAGAC CAAGGAACAC GTGCCTTTAT 600
 CTCTAACCTT TATAGCGGTT CTGTAACAGA TGAAAAAGTT AGCAAATATA CAACTGATGA 660
 TCCTAAATTC GTCAAAGGTC TTGAAAAAGC AACTAGCTGG ATTAAAGACA ATTTGATCAA 720
 TAATGGTTCA CAATTTGACG GTGGGGCAGA TATCCAAAAC TTTGCCAACG GTCAAACATC 780
 TTACACAATC CTTTGGGCAC CAGCTCAAAA TGGTATCCAA GCTAAACTTT TAGAAGCAAG 840
 TAAGGTAGAA GTGGTAGAAG TACCATTCCC ATCAGACGAA GGTAAGCCAG CTCTTGAGTA 900
 CCTTGTAAC GGGTTTGCAG TATTCAACAA TAAAGACGAC AAGAAAGTCG CTGCATCTAA 960
 GAAATTCATC CAGTTTATCG CAGATGACAA GGAGTGGGGA CCTAAAGACG TAGTTTCGTAC 1020
 AGGTGCTTTC CCAGTCCGTA CTTCAATTGG AAACTTTAT GAAGACAAAC GCATGGAAAC 1080
 AATCAGCGGC TGGACTCAAT ACTACTCACC ATACTACAAC ACTATTGATG GATTGCTGA 1140
 AATGAGAACA CTTTGGTTCC CAATGTTGCA ATCTGTATCA AATGGTGACG AAAAACCAGC 1200
 AGATGCTTTG AAAGCCTTCA CTGAAAAAGC GAACGAAACA ATCAAAAAAG CTATGAAACA 1260
 A 1261

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gly Asn Ser Gly Gly Ser Lys Asp Ala Ala Lys Ser Gly Gly Asp Gly
 1 5 10 15
 Ala Lys Thr Glu Ile Thr Trp Trp Ala Phe Pro Val Phe Thr Gln Glu
 20 25 30
 Lys Thr Gly Asp Gly Val Gly Thr Tyr Glu Lys Ser Ile Ile Glu Ala
 35 40 45
 Phe Glu Lys Ala Asn Pro Asp Ile Lys Val Lys Leu Glu Thr Ile Asp
 50 55 60
 Phe Lys Ser Gly Pro Glu Lys Ile Thr Thr Ala Ile Glu Ala Gly Thr
 65 70 75 80
 Ala Pro Asp Val Leu Phe Asp Ala Pro Gly Arg Ile Ile Gln Tyr Gly
 85 90 95
 Lys Asn Gly Lys Leu Ala Glu Leu Asn Asp Leu Phe Thr Asp Glu Phe
 100 105 110
 Val Lys Asp Val Asn Asn Glu Asn Ile Val Gln Ala Ser Lys Ala Gly
 115 120 125
 Asp Lys Ala Tyr Met Tyr Pro Ile Ser Ser Ala Pro Phe Tyr Met Ala
 130 135 140
 Met Asn Lys Lys Met Leu Glu Asp Ala Gly Val Ala Asn Leu Val Lys
 145 150 155 160
 Glu Gly Trp Thr Thr Asp Asp Phe Glu Lys Val Leu Lys Ala Leu Lys
 165 170 175
 Asp Lys Gly Tyr Thr Pro Gly Ser Leu Phe Ser Ser Gly Gln Gly Gly
 180 185 190
 Asp Gln Gly Thr Arg Ala Phe Ile Ser Asn Leu Tyr Ser Gly Ser Val
 195 200 205
 Thr Asp Glu Lys Val Ser Lys Tyr Thr Thr Asp Asp Pro Lys Phe Val
 210 215 220
 Lys Gly Leu Glu Lys Ala Thr Ser Trp Ile Lys Asp Asn Leu Ile Asn
 225 230 235 240
 Asn Gly Ser Gln Phe Asp Gly Gly Ala Asp Ile Gln Asn Phe Ala Asn
 245 250 255
 Gly Gln Thr Ser Tyr Thr Ile Leu Trp Ala Pro Ala Gln Asn Gly Ile
 260 265 270
 Gln Ala Lys Leu Leu Glu Ala Ser Lys Val Glu Val Val Glu Val Pro

275	280	285
Phe Pro Ser Asp Glu Gly Lys	Pro Ala Leu Glu Tyr	Leu Val Asn Gly
290	295	300
Phe Ala Val Phe Asn Asn Lys	Asp Asp Lys Lys Val	Ala Ala Ser Lys
305	310	315 320
Lys Phe Ile Gln Phe Ile Ala	Asp Asp Lys Glu Trp Gly	Pro Lys Asp
325	330	335
Val Val Arg Thr Gly Ala Phe	Pro Val Arg Thr Ser Phe	Gly Lys Leu
340	345	350
Tyr Glu Asp Lys Arg Met Glu	Thr Ile Ser Gly Trp Thr	Gln Tyr Tyr
355	360	365
Ser Pro Tyr Tyr Asn Thr Ile	Asp Gly Phe Ala Glu Met	Arg Thr Leu
370	375	380
Trp Phe Pro Met Leu Gln Ser	Val Ser Asn Gly Asp Glu	Lys Pro Ala
385	390	395 400
Asp Ala Leu Lys Ala Phe Thr	Glu Lys Ala Asn Glu Thr	Ile Lys Lys
405	410	415
Ala Met Lys Gln		
420		

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 658 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TTCACAAGAA AAAACAAAA ATGAAGATGG AGAACTAAG ACAGAACAGA CAGCCAAAGC	60
TGATGGAACA GTCGGTAGTA AGTCTCAAGG AGCTGCCCAG AAGAAAGCAG AAGTGGTCAA	120
TAAAGGTGAT TACTACAGCA TTCAAGGGAA ATACGATGAA ATCATCGTAG CCAACAAACA	180
CTATCCATG TCTAAAGACT ATAATCCAGG GGAAAATCCA ACAGCCAAGG CAGAGTTGGT	240
CAAATCATC AAAGCGATGC AAGAGGCAGG TTTCCCTATT AGTGATCATT ACAGTGGTTT	300
TAGAAGTTAT GAAACTCAGA CCAAGCTCTA TCAAGATTAT GTCAACCAAG ATGGAAAGGC	360
AGCAGCTGAC CGTTACTCTG CCCGTCCTGG CTATAGCGAA CACCAGACAG GCTTGGCCTT	420
TGATGTGATT GGGACTGATG GTGATTGGT GACAGAAGAA AAAGCAGCCC AATGGCTCTT	480
GGATCATGCA GCTGATTATG GCTTTGTGT CCGTTATCTC AAAGGCAAGG AAAAGGAAAC	540
AGGCTATATG GCTGAAGAAT GGCACCTGCG TTATGTAGGA AAAGAAGCTA AAGAAATTGC	600
TGCAAGTGGT CTCAGTTTGG AAGAATACTA TGGCTTTGAA GCGGAGACT ACGTCGAT	658

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ser Gln Glu Lys Thr Lys Asn Glu Asp Gly Glu Thr Lys Thr Glu Gln
 1 5 10 15
 Thr Ala Lys Ala Asp Gly Thr Val Gly Ser Lys Ser Gln Gly Ala Ala
 20 25 30
 Gln Lys Lys Ala Glu Val Val Asn Lys Gly Asp Tyr Tyr Ser Ile Gln
 35 40 45
 Gly Lys Tyr Asp Glu Ile Ile Val Ala Asn Lys His Tyr Pro Leu Ser
 50 55 60
 Lys Asp Tyr Asn Pro Gly Glu Asn Pro Thr Ala Lys Ala Glu Leu Val
 65 70 75 80
 Lys Leu Ile Lys Ala Met Gln Glu Ala Gly Phe Pro Ile Ser Asp His
 85 90 95
 Tyr Ser Gly Phe Arg Ser Tyr Glu Thr Gln Thr Lys Leu Tyr Gln Asp
 100 105 110
 Tyr Val Asn Gln Asp Gly Lys Ala Ala Ala Asp Arg Tyr Ser Ala Arg
 115 120 125
 Pro Gly Tyr Ser Glu His Gln Thr Gly Leu Ala Phe Asp Val Ile Gly
 130 135 140
 Thr Asp Gly Asp Leu Val Thr Glu Glu Lys Ala Ala Gln Trp Leu Leu
 145 150 155 160
 Asp His Ala Ala Asp Tyr Gly Phe Val Val Arg Tyr Leu Lys Gly Lys
 165 170 175
 Glu Lys Glu Thr Gly Tyr Met Ala Glu Glu Trp His Leu Arg Tyr Val
 180 185 190
 Gly Lys Glu Ala Lys Glu Ile Ala Ala Ser Gly Leu Ser Leu Glu Glu
 195 200 205
 Tyr Tyr Gly Phe Glu Gly Gly Asp Tyr Val Asp
 210 215

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GAAAGGTCTG TGGTCAAATA ATCTTACCTG CGGTTATGAT GAAAAAATAA TCTTGAAAA 60
TATAAATATA AAAATACCTG AAGAAAAAAT ATCAGTTATT ATTGGGTCAA ATGGTTGTGG 120
GAAATCAACA CTCATTAAAA CCTTGTCTCG ACTTATAAAG CCATTAGAGG GAGAAGTATT 180
GCTTGATAAT AAATCAATTA ATTCTTATAA AGAAAAAGAT TTAGCAAAAC ACATAGCTAT 240
ATTACCTCAA TCTCCAATAA TCCCTGAATC AATAACAGTA GCTGATCTTG TAAGCCGTGG 300
TCGTTTCCCC TACAGAAAGC CTTTAAAGAG TCTTGAAAA GATGACCTTG AAATAATAAA 360
CAGATCAATG GTTAAGGCCA ATGTTGAAGA TCTAGCAAAT AACCTAGTTG AAGAACTTTC 420
TGGGGGTCAA AGGCAAAGAG TATGGATAGC TCTAGCCCTA GCCCAAGATA CAAGTATCCT 480
ACTTTTAGAT GAGCCAATA CTTACTTGGG TATCTCATAT CAAATAGAAC TATTAGACCT 540
CTTGACTGAT CTAAACCAAA AATATAAGAC AACCATTTGC ATGATTTTGC ACGATATAAA 600
TCTAACAGCA AGATACGCTG ATTACCTATT TGCAATTAAA GAAGGTAAAC TTGTTGCAGA 660
GGGAAAGCCT GAAGATATAC TAAATGATAA ACTAGTTAAA GATATCTTTA ATCTTGAAGC 720
AAAAATTATA CGTGACCCTA TTTCCAATTC GCCTCTAATG ATTCCTATTG GCAAGCACCA 780
TGTTAACTCT 790

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 262 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Lys Gly Leu Trp Ser Asn Asn Leu Thr Cys Gly Tyr Asp Glu Lys Ile
1 5 10 15
Ile Leu Glu Asn Ile Asn Ile Lys Ile Pro Glu Glu Lys Ile Ser Val
20 25 30
Ile Ile Gly Ser Asn Gly Cys Gly Lys Ser Thr Leu Ile Lys Thr Leu
35 40 45
Ser Arg Leu Ile Lys Pro Leu Glu Gly Glu Val Leu Leu Asp Asn Lys
50 55 60
Ser Ile Asn Ser Tyr Lys Glu Lys Asp Leu Ala Lys His Ile Ala Ile
65 70 75 80

Leu Pro Gln Ser Pro Ile Ile Pro Glu Ser Ile Thr Val Ala Asp Leu
 85 90 95
 Val Ser Arg Gly Arg Phe Pro Tyr Arg Lys Pro Phe Lys Ser Leu Gly
 100 105 110
 Lys Asp Asp Leu Glu Ile Ile Asn Arg Ser Met Val Lys Ala Asn Val
 115 120 125
 Glu Asp Leu Ala Asn Asn Leu Val Glu Glu Leu Ser Gly Gly Gln Arg
 130 135 140
 Gln Arg Val Trp Ile Ala Leu Ala Leu Ala Gln Asp Thr Ser Ile Leu
 145 150 155 160
 Leu Leu Asp Glu Pro Thr Thr Tyr Leu Asp Ile Ser Tyr Gln Ile Glu
 165 170 175
 Leu Leu Asp Leu Leu Thr Asp Leu Asn Gln Lys Tyr Lys Thr Thr Ile
 180 185 190
 Cys Met Ile Leu His Asp Ile Asn Leu Thr Ala Arg Tyr Ala Asp Tyr
 195 200 205
 Leu Phe Ala Ile Lys Glu Gly Lys Leu Val Ala Glu Gly Lys Pro Glu
 210 215 220
 Asp Ile Leu Asn Asp Lys Leu Val Lys Asp Ile Phe Asn Leu Glu Ala
 225 230 235 240
 Lys Ile Ile Arg Asp Pro Ile Ser Asn Ser Pro Leu Met Ile Pro Ile
 245 250 255
 Gly Lys His His Val Ser
 260

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 781 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AAACTCAGAA AAGAAAGCAG ACAATGCAAC AACTATCAAA ATCGCAACTG TTAACCGTAG	60
CGGTTCTGAA GAAAAACGTT GGGACAAAAT CCAAGAATTG GTTAAAAAAG ACGGAATTAC	120
CTTGGAATTT ACAGAGTTCA CAGACTACTC ACAACCAAAC AAAGCAACTG CTGATGGCGA	180
AGTAGATTTG AACGCTTTCC AACACTATAA CTTCTTGAAC AACTGGAACA AAGAAAACGG	240
AAAAGACCTT GTAGCGATTG CAGATACTTA CATCTCTCCA ATCCGCCTTT ACTCAGGTTT	300
GAATGGAAGT GCCAACAAGT AACTAAAGT AGAAGACATC CCAGCAAACG GAGAAATCCG	360
TGTACCGAAT GACGCTACAA ACGAAAGCCG TCGCTTTAT TTGCTTCAAT CAGCTGGCTT	420

GATTAAATTG GATGTTTCTG GAACTGCTCT TGCAACAGTT GCCAACATCA AAGAAAATCC 480
 AAAGAACTTG AAAATCACTG AATTGGACGC TAGCCAAACA GCTCGTTCAT TGTCATCAGT 540
 TGACGCTGCC GTTGTAACA ATACCTTCGT TACAGAAGCA AAATTGGACT ACAAGAAATC 600
 ACTTTTCAAA GAACAAGCTG ATGAAAACATC AAAACAATGG TACAACATCA TTGTTGCAAA 660
 AAAAGATTGG GAAACATCAC CTAAGGCTGA TGCTATCAAG AAAGTAATCG CAGCTTACCA 720
 CACAGATGAC GTGAAAAAAG TTATCGAAGA ATCATCAGAT GGTTCGGATC AACCAGTTTG 780
 G 781

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asn Ser Glu Lys Lys Ala Asp Asn Ala Thr Thr Ile Lys Ile Ala Thr
 1 5 10 15
 Val Asn Arg Ser Gly Ser Glu Glu Lys Arg Trp Asp Lys Ile Gln Glu
 20 25 30
 Leu Val Lys Lys Asp Gly Ile Thr Leu Glu Phe Thr Glu Phe Thr Asp
 35 40 45
 Tyr Ser Gln Pro Asn Lys Ala Thr Ala Asp Gly Glu Val Asp Leu Asn
 50 55 60
 Ala Phe Gln His Tyr Asn Phe Leu Asn Asn Trp Asn Lys Glu Asn Gly
 65 70 75 80
 Lys Asp Leu Val Ala Ile Ala Asp Thr Tyr Ile Ser Pro Ile Arg Leu
 85 90 95
 Tyr Ser Gly Leu Asn Gly Ser Ala Asn Lys Tyr Thr Lys Val Glu Asp
 100 105 110
 Ile Pro Ala Asn Gly Glu Ile Ala Val Pro Asn Asp Ala Thr Asn Glu
 115 120 125
 Ser Arg Ala Leu Tyr Leu Leu Gln Ser Ala Gly Leu Ile Lys Leu Asp
 130 135 140
 Val Ser Gly Thr Ala Leu Ala Thr Val Ala Asn Ile Lys Glu Asn Pro
 145 150 155 160
 Lys Asn Leu Lys Ile Thr Glu Leu Asp Ala Ser Gln Thr Ala Arg Ser
 165 170 175
 Leu Ser Ser Val Asp Ala Ala Val Val Asn Asn Thr Phe Val Thr Glu

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 cont.

180	185	190
Ala Lys Leu Asp Tyr Lys Lys Ser Leu Phe Lys Glu Gln Ala Asp Glu		
195	200	205
Asn Ser Lys Gln Trp Tyr Asn Ile Ile Val Ala Lys Lys Asp Trp Glu		
210	215	220
Thr Ser Pro Lys Ala Asp Ala Ile Lys Lys Val Ile Ala Ala Tyr His		
225	230	235
Thr Asp Asp Val Lys Lys Val Ile Glu Glu Ser Ser Asp Gly Leu Asp		
245	250	255
Gln Pro Val Trp		
260		

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

a' cont.

TTCGAAAGGG TCAGAAGGTG CAGACCTTAT CAGCATGAAA GGGGATGTCA TTACAGAACA	60
TCAATTTTAT GAGCAAGTGA AAAGCAACCC TTCAGCCCAA CAAGTCTTGT TAAATATGAC	120
CATCCAAAAA GTTTTGTGAAA AACAATATGG CTCAGAGCTT GATGATAAAG AGGTTGATGA	180
TACTATTGCC GAAGAAAAAA AACAATATGG CGAAACTAC CAACGTGTCT TGTCACAAGC	240
AGGTATGACT CTTGAAACAC GTAAAGCTCA AATTCGTACA AGTAAATTAG TTGAGTTGGC	300
AGTTAAGAAG GTAGCAGAAG CTGAATTGAC AGATGAAGCC TATAAGAAAG CCTTTGATGA	360
GTACACTCCA GATGTAACGG CTCAAATCAT CCGTCTTAAT AATGAAGATA AGGCCAAAGA	420
AGTTCTCGAA AAAGCCAAGG CAGAAGGTGC TGATTTTGCT CAATTAGCCA AAGATAATTC	480
AACTGATGAA AAAACAAAAG AAAATGGTGG AGAAATTACC TTTGATTCTG CTTCAACAGA	540
AGTACCTGGA GCAAGTCCAA AAAAGCCGCT TTTGCTTTT AGATGTGGGA TGGTGTCTCT	600
GGATGTGGAT TACAGCAACT GGGGCACACC AAGCCTACAG	640

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser Lys Gly Ser Glu Gly Ala Asp Leu Ile Ser Met Lys Gly Asp Val
 1 5 10 15
 Ile Thr Glu His Gln Phe Tyr Glu Gln Val Lys Ser Asn Pro Ser Ala
 20 25 30
 Gln Gln Val Leu Leu Asn Met Thr Ile Gln Lys Val Phe Glu Lys Gln
 35 40 45
 Tyr Gly Ser Glu Leu Asp Asp Lys Glu Val Asp Asp Thr Ile Ala Glu
 50 55 60
 Glu Lys Lys Gln Tyr Gly Glu Asn Tyr Gln Arg Val Leu Ser Gln Ala
 65 70 75 80
 Gly Met Thr Leu Glu Thr Arg Lys Ala Gln Ile Arg Thr Ser Lys Leu
 85 90 95
 Val Glu Leu Ala Val Lys Lys Val Ala Glu Ala Glu Leu Thr Asp Glu
 100 105 110
 Ala Tyr Lys Lys Ala Phe Asp Glu Tyr Thr Pro Asp Val Thr Ala Gln
 115 120 125
 Ile Ile Arg Leu Asn Asn Glu Asp Lys Ala Lys Glu Val Leu Glu Lys
 130 135 140
 Ala Lys Ala Glu Gly Ala Asp Phe Ala Gln Leu Ala Lys Asp Asn Ser
 145 150 155 160
 Thr Asp Glu Lys Thr Lys Glu Asn Gly Gly Glu Ile Thr Phe Asp Ser
 165 170 175
 Ala Ser Thr Glu Val Pro Gly Ala Ser Pro Lys Lys Pro Leu Phe Ala
 180 185 190
 Phe Arg Cys Gly Met Val Phe Leu Asp Val Asp Tyr Ser Asn Trp Gly
 195 200 205
 Thr Pro Ser Leu Gln
 210

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 631 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GGGGATGGCA GCTTTTAAAA ATCCTAACAA TCAATACAAA GCTATTACAA TTGCTCAAAC 60
 TCTAGGTGAT GATGCTTCTT CAGAGGAATT GGCTGGTAGA TATGGTCTG CTGTTCAGTG 120
 TACAGAAGTG ACTGCCTCAA ACCTTTCAAC AGTTAAAACT AAAGCTACGG TTGTAGAAAA 180

ACCACTGAAA GATTTTAGAG CGTCTACGTC TGATCAGTCT GGTGGGTGG AATCTAATGG 240
 TAAATGGTAT TTCTATGAGT CTGGTGATGT GAAGACAGGT TGGGTGAAAA CAGATGGTAA 300
 ATGGTACTAT TTGAATGACT TAGGTGTCAT GCAGACTGGA TTTGTAAAAT TTTCTGGTAG 360
 CTGGTATTAC TTGAGCAATT CAGGTGCTAT GTTTACAGGC TGGGGAACAG ATGGTAGCAG 420
 ATGGTTCTAC TTTGACGGCT CAGGAGCTAT GAAGACAGGC TGGTACAAGG AAAATGGCAC 480
 TTGGTATTAC CTTGACGAAG CAGGTATCAT GAAGACAGGT TGGTTTAAAG TCGGACCACA 540
 CTGGTACTAT GCCTACGGTT CAGGAGCTTT GGCTGTGAGC ACAACAACAC CAGATGGTTA 600
 CCGTGTAAT GGTAATGGTG AATGGGTAAA C 631

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Met Ala Ala Phe Lys Asn Pro Asn Asn Gln Tyr Lys Ala Ile Thr
 1 5 10 15
 Ile-Ala Gln Thr Leu Gly Asp Asp Ala Ser Ser Glu Glu Leu Ala Gly
 20 25 30
 Arg Tyr Gly Ser Ala Val Gln Cys Thr Glu Val Thr Ala Ser Asn Leu
 35 40 45
 Ser Thr Val Lys Thr Lys Ala Thr Val Val Glu Lys Pro Leu Lys Asp
 50 55 60
 Phe Arg Ala Ser Thr Ser Asp Gln Ser Gly Trp Val Glu Ser Asn Gly
 65 70 75 80
 Lys Trp Tyr Phe Tyr Glu Ser Gly Asp Val Lys Thr Gly Trp Val Lys
 85 90 95
 Thr Asp Gly Lys Trp Tyr Tyr Leu Asn Asp Leu Gly Val Met Gln Thr
 100 105 110
 Gly Phe Val Lys Phe Ser Gly Ser Trp Tyr Tyr Leu Ser Asn Ser Gly
 115 120 125
 Ala Met Phe Thr Gly Trp Gly Thr Asp Gly Ser Arg Trp Phe Tyr Phe
 130 135 140
 Asp Gly Ser Gly Ala Met Lys Thr Gly Trp Tyr Lys Glu Asn Gly Thr
 145 150 155 160
 Trp Tyr Tyr Leu Asp Glu Ala Gly Ile Met Lys Thr Gly Trp Phe Lys
 165 170 175

Val Gly Pro His Trp Tyr Tyr Ala Tyr Gly Ser Gly Ala Leu Ala Val
 180 185 190

Ser Thr Thr Thr Pro Asp Gly Tyr Arg Val Asn Gly Asn Gly Glu Trp
 195 200 205

Val Asn
 210

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

AGACGAGCAA AAAATTAAGC AAGCAGAAGC GGAAGTTGAG AGTAAACAAG CTGAGGCTAC 60
 AAGGTTAAAA AAAATCAAGA CAGATCGTGA AGAAGCAGAA GAAGAAGCTA AACGAAGAGC 120
 AGATGCTAAA GAGCAAGGTA AACCAAAGGG GCGGGCAAAA CGAGGAGTTC CTGGAGAGCT 180
 AGCAACACCT GATAAAAAAG AAAATGATGC GAAGTCTTCA GATTCTAGCG TAGGTGAAGA 240
 AACTCTTCCA AGCCCATCCC TGAAACCAGA AAAAAAGGTA GCAGAAGCTG AGAAGAAGGT 300
 TGAAGAAGCT AAGAAAAAAG CCGAGGATCA AAAAGAAGAA GATCGCCGTA ACTACCCAAC 360
 CAATACCTTAC AAAACGCTTG AACTTGAAAT TGCTGAGTCC GATGTGGAAG TTAAAAAAGC 420
 GGAGCTTGAA CTAGTAAAAG AGGAAGCTAA GGAACCTCGA AACGAGGAAA AAGTTAAGCA 480
 AGCAAAAGCG GAAGTTGAGA GTAAAAAAGC TGAGGCTACA AGGTTAGAAA AAATCAAGAC 540
 AGATCGTAAA AAAGCAGAAG AAGAAGCTAA ACGAAAAGCA GCAGAAGAAG ATAAAGTTAA 600
 AGAAAAACCA GCTGAACAAC CACAACCAGC GCCGGCTCCA AAAGCAGAAA AACCAGCTCC 660
 AGCTCCAAAA CCAGAGAATC CAGCTGAACA ACCAAAAGCA GAAAAACCAG CTGATCAACA 720
 AGCTGAAGAA GACTATGCTC GTAGATCAGA AGAAGAATAT AATCGCTTGA CTCAACAGCA 780
 ACCGCCAAAA ACTGAAAAAC CAGCACAACC ATCTACTCCA AAAACAGGCT GGAAACAAGA 840
 AAACGGTATG TGGTACTTCT ACAATACTGA TGGTTCAATG GCGACAGGAT GGCTCCAAAA 900
 CAATGGCTCA TGGTACTACC TCAACAGCAA TGGCGCTATG GCGACAGGAT GGCTCCAAAA 960
 CAATGGTTCA TGGTACTATC TAAACGCTAA TGGTTCAATG GCAACAGGAT GGCTCCAAAA 1020
 CAATGGTTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAATA 1080
 CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAATA 1140
 CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTGATATG GCGACAGGTT GGGTGAAAGA 1200
 TGGAGATACC TGGTACTATC TTGAAGCATC AGGTGCTATG AAAGCAAGCC AATGGTTCAA 1260

AGTATCAGAT AAATGGTACT ATGTCAATGG CTCAGGTGCC CTTGCAGTCA ACACAACTGT 1320

AGATGGCTAT GGAGTCAATG CCAATGGTGA ATGGGTAAAC 1360

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Asp Glu Gln Lys Ile Lys Gln Ala Glu Ala Glu Val Glu Ser Lys Gln
1 5 10 15

Ala Glu Ala Thr Arg Leu Lys Lys Ile Lys Thr Asp Arg Glu Glu Ala
20 25 30

Glu Glu Glu Ala Lys Arg Arg Ala Asp Ala Lys Glu Gln Gly Lys Pro
35 40 45

Lys Gly Arg Ala Lys Arg Gly Val Pro Gly Glu Leu Ala Thr Pro Asp
50 55 60

Lys Lys Glu Asn Asp Ala Lys Ser Ser Asp Ser Ser Val Gly Glu Glu
65 70 75 80

Thr Leu Pro Ser Pro Ser Leu Lys Pro Glu Lys Lys Val Ala Glu Ala
85 90 95

Glu Lys Lys Val Glu Glu Ala Lys Lys Lys Ala Glu Asp Gln Lys Glu
100 105 110

Glu Asp Arg Arg Asn Tyr Pro Thr Asn Thr Tyr Lys Thr Leu Glu Leu
115 120 125

Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala Glu Leu Glu Leu
130 135 140

Val Lys Glu Glu Ala Lys Glu Pro Arg Asn Glu Lys Val Lys Gln
145 150 155 160

Ala Lys Ala Glu Val Glu Ser Lys Lys Ala Glu Ala Thr Arg Leu Glu
165 170 175

Lys Ile Lys Thr Asp Arg Lys Lys Ala Glu Glu Glu Ala Lys Arg Lys
180 185 190

Ala Ala Glu Glu Asp Lys Val Lys Glu Lys Pro Ala Glu Gln Pro Gln
195 200 205

Pro Ala Pro Ala Pro Lys Ala Glu Lys Pro Ala Pro Ala Pro Lys Pro
210 215 220

Glu Asn Pro Ala Glu Gln Pro Lys Ala Glu Lys Pro Ala Asp Gln Gln

a' cont.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CTGTGGTGAG	GAAGAAACTA	AAAAGACTCA	AGCAGCACAA	CAGCCAAAAC	AACAAACGAC	60
TGTACAACAA	ATTGCTGTTG	GAAAAGATGC	TCCAGACTTC	ACAATTGCAAT	CCATGGATGG	120
CAAAGAAGTT	AAGTTATCTG	ATTTTAAGGG	TAAAAAGGTT	TACTTGAAGT	TTTGGGCTTC	180
ATGGTGTGGT	CCATGCAAGA	AAAGTATGCC	AGAGTTGATG	GAAGTAGCGG	CGAAACCAGA	240

TCGTGATTTC GAAATTCTTA CTGTCATTGC ACCAGGAATT CAAGGTGAAA AACTGTTGA 300
 GCAATTCCCA CAATGGTTCC AGGAACAAGG ATATAAGGAT ATCCCAGTTC TTTATGATAC 360
 CAAAGCAACC ACTTCCAAGC TTATCAAATT CGAAGCATTC CTACAGAATA TT 412

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Cys Gly Glu Glu Thr Lys Lys Thr Gln Ala Ala Gln Gln Pro Lys
 1 5 10 15
 Gln Gln Thr Thr Val Gln Gln Ile Ala Val Gly Lys Asp Ala Pro Asp
 20 25 30
 Phe Thr Leu Gln Ser Met Asp Gly Lys Glu Val Lys Leu Ser Asp Phe
 35 40 45
 Lys Gly Lys Lys Val Tyr Leu Lys Phe Trp Ala Ser Trp Cys Gly Pro
 50 55 60
 Cys Lys Lys Ser Met Pro Glu Leu Met Glu Leu Ala Ala Lys Pro Asp
 65 70 75 80
 Arg Asp Phe Glu Ile Leu Thr Val Ile Ala Pro Gly Ile Gln Gly Glu
 85 90 95
 Lys Thr Val Glu Gln Phe Pro Gln Trp Phe Gln Glu Gln Gly Tyr Lys
 100 105 110
 Asp Ile Pro Val Leu Tyr Asp Thr Lys Ala Thr Thr Ser Lys Leu Ile
 115 120 125
 Lys Phe Glu Ala Phe Leu Gln Asn Ile
 130 135

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GACTTTTAAC AATAAACTA TTGAAGAGTT GCACAATCTC CTTGTCTCTA AGGAAATTTC 60

TGCAACAGAA TTGACCCAAG CAACACTTGA AAATATCAAG TCTCGTGAGG AAGCCCTCAA 120
 TTCATTTGTC ACCATCGCTG AGGAGCAAGC TCTTGTTCAG GCTAAAGCCA TTGATGAAGC 180
 tGGAATTGAT GCTGACAATG TCCTTTCAGG AATTCCACTT GCTGTTAAGG ATAACATCTC 240
 TACAGACGGT ATTCTCACAA CTGCTGCCTC AAAAAAGCTC TACAACTATG AGCCAATCTT 300
 TGATGCGACa gCTgTTGCCA ATGCAAAAAC CAAGGCATG ATTGTCGTTG GAAAGACCAA 360
 CATGGACGAA TTTGCTATGG GTGGTTCAGG tGAAACTTCA CACTACGGAG CAACTAAAAA 420
 CGCTTGGAAC CACAGCAAGG TTCCTGGTGG GTCATCAAGT GGTTCGCGG CAGCTGTAGC 480
 CTCAGGACAA GTTCGCTTGT CACTTGGTTC TGATACTGGT GGTTCATCC GCCAACCTGC 540
 TGCCCTCAAC GGAATCGTTG GTCTCAACC AACCTACGGA ACAGTTTCAC GTTTCGGTCT 600
 CATTGCCTTT GGTAGCTCAT TAGACCAGAT TGGACCTTTT GCTCCTACTG TTAAGGAAAA 660
 TGCCCTCTTG CTCAACGCTA TTGCCAGCGA AGATGCTAAA GACTCTACTT CTGCTCCTGT 720
 CCGCATCGCC GACTTTACTT CAAAAATCGG CCAAGACATC AAGGGTATGA AAATCGCTTT 780
 GCCTAAGGAA TACCTAGGCG AAGGAATTGA TCCAGAGGTT AAGGAAACAA TCTTAAACGC 840
 GGCCAAACAC TTTGAAAAAT TGGGTGCTAT CGTCGAAGAA GTCAGCCTTC CTCACTCTAA 900
 ATACGGTGTT GCCGTTTATT ACATCATCGC TTCATCAGAA GCTTCATCAA ACTTGCAACG 960
 CTTGACGGT ATCCGTTACG GCTATCGCGC AGAAGATGCA ACCAACCTTG ATGAAATCTA 1020
 TGTAACAGC CGAAGCCAAG GTTTTGGTGA AGAGGTAAAA CGTCGTATCA TGCTGGGTAC 1080
 TTTCACTCTT TCATCAGGTT ACTATGATGC CTAATAACAA AAGGCTGGTC AAGTCCGTAC 1140
 CCTCATATT CAAGATTTTCG AAAAAAGCTT CGCGGATTAC GATTTGATTT TGGGTCCAAC 1200
 TGCTCCAAGT GTTGCTTATG ACTTGGATTG TCTCAACCAT GACCCAGTTG CCATGTACTT 1260
 AGCCGACCTA TTGACCATAC CTGTAAACTT GGCAGGACTG CCTGGAATTT CGATTCCTGC 1320
 TGGATTCTCT CAAGGTCTAC CTGTCGGACT CCAATTGATT GGTCCCAAGT ACTCTGAGGA 1380
 AACCATTAC CAAGCTGCTG CTGCTTTTGA AGCAACAACA GACTACCACA AACAACAACC 1440
 CGTGATTTT GGAGGTGACA AC 1462

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 487 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Thr Phe Asn Asn Lys Thr Ile Glu Glu Leu His Asn Leu Leu Val Ser
 1 5 10 15
 Lys Glu Ile Ser Ala Thr Glu Leu Thr Gln Ala Thr Leu Glu Asn Ile
 20 25 30
 Lys Ser Arg Glu Glu Ala Leu Asn Ser Phe Val Thr Ile Ala Glu Glu
 35 40 45
 Gln Ala Leu Val Gln Ala Lys Ala Ile Asp Glu Ala Gly Ile Asp Ala
 50 55 60
 Asp Asn Val Leu Ser Gly Ile Pro Leu Ala Val Lys Asp Asn Ile Ser
 65 70 75 80
 Thr Asp Gly Ile Leu Thr Thr Ala Ala Ser Lys Met Leu Tyr Asn Tyr
 85 90 95
 Glu Pro Ile Phe Asp Ala Thr Ala Val Ala Asn Ala Lys Thr Lys Gly
 100 105 110
 Met Ile Val Val Gly Lys Thr Asn Met Asp Glu Phe Ala Met Gly Gly
 115 120 125
 Ser Gly Glu Thr Ser His Tyr Gly Ala Thr Lys Asn Ala Trp Asn His
 130 135 140
 Ser Lys Val Pro Gly Gly Ser Ser Ser Gly Ser Ala Ala Ala Val Ala
 145 150 155 160
 Ser Gly Gln Val Arg Leu Ser Leu Gly Ser Asp Thr Gly Gly Ser Ile
 165 170 175
 Arg Gln Pro Ala Ala Phe Asn Gly Ile Val Gly Leu Lys Pro Thr Tyr
 180 185 190
 Gly Thr Val Ser Arg Phe Gly Leu Ile Ala Phe Gly Ser Ser Leu Asp
 195 200 205
 Gln Ile Gly Pro Phe Ala Pro Thr Val Lys Glu Asn Ala Leu Leu Leu
 210 215 220
 Asn Ala Ile Ala Ser Glu Asp Ala Lys Asp Ser Thr Ser Ala Pro Val
 225 230 235 240
 Arg Ile Ala Asp Phe Thr Ser Lys Ile Gly Gln Asp Ile Lys Gly Met
 245 250 255
 Lys Ile Ala Leu Pro Lys Glu Tyr Leu Gly Glu Gly Ile Asp Pro Glu
 260 265 270
 Val Lys Glu Thr Ile Leu Asn Ala Ala Lys His Phe Glu Lys Leu Gly
 275 280 285
 Ala Ile Val Glu Glu Val Ser Leu Pro His Ser Lys Tyr Gly Val Ala
 290 295 300
 Val Tyr Tyr Ile Ile Ala Ser Ser Glu Ala Ser Ser Asn Leu Gln Arg
 305 310 315 320
 Phe Asp Gly Ile Arg Tyr Gly Tyr Arg Ala Glu Asp Ala Thr Asn Leu
 325 330 335

a'
 cont.

Asp Glu Ile Tyr Val Asn Ser Arg Ser Gln Gly Phe Gly Glu Glu Val
 340 345 350
 Lys Arg Arg Ile Met Leu Gly Thr Phe Ser Leu Ser Ser Gly Tyr Tyr
 355 360 365
 Asp Ala Tyr Tyr Lys Lys Ala Gly Gln Val Arg Thr Leu Ile Ile Gln
 370 375 380
 Asp Phe Glu Lys Val Phe Ala Asp Tyr Asp Leu Ile Leu Gly Pro Thr
 385 390 395 400
 Ala Pro Ser Val Ala Tyr Asp Leu Asp Ser Leu Asn His Asp Pro Val
 405 410 415
 Ala Met Tyr Leu Ala Asp Leu Leu Thr Ile Pro Val Asn Leu Ala Gly
 420 425 430
 Leu Pro Gly Ile Ser Ile Pro Ala Gly Phe Ser Gln Gly Leu Pro Val
 435 440 445
 Gly Leu Gln Leu Ile Gly Pro Lys Tyr Ser Glu Glu Thr Ile Tyr Gln
 450 455 460
 Ala Ala Ala Ala Phe Glu Ala Thr Thr Asp Tyr His Lys Gln Gln Pro
 465 470 475 480
 Val Ile Phe Gly Gly Asp Asn
 485

a' Cont.
 (2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 433 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CTTTACAGGT AAACAACCTAC AAGTCGGCGA CAAGGCGCTT GATTTTCTC TTACTACAAC	60
AGATCTTTCT AAAAAATCTC TGGCTGATTT TGATGGCAAG AAAAAAGTCT TGAGTGTCTG	120
TCCTTCTATC GATACAGGCA TCTGCTCAAC TCAAACACGT CGTTTTAATG AAGAATTGGC	180
TGGACTGGAC AACACGGTCG TATTGACTGT TTCAATGGAC CTACCTTTTG CTCAAAAACG	240
TTGGTGCGGT GCTGAAGGCC TTGACAATGC CATTATGCTT TCAGACTACT TTGACCATTC	300
TTTCGGGCGC GATTATGCCC TCTTGATCAA CGAATGGCAC CTATTAGCAC GCGCAGTCTT	360
TGTCCTCGAT ACTGACAATA CGATTGCTA CGTTGAATAC GTGGATAATA TCAATTCTGA	420
GCCAAACTTC GAA	433

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 144 amino acids
 - (B) TYPE: amino acid
- V54

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Phe Thr Gly Lys Gln Leu Gln Val Gly Asp Lys Ala Leu Asp Phe Ser
1 5 10 15
Leu Thr Thr Thr Asp Leu Ser Lys Lys Ser Leu Ala Asp Phe Asp Gly
20 25 30
Lys Lys Lys Val Leu Ser Val Val Pro Ser Ile Asp Thr Gly Ile Cys
35 40 45
Ser Thr Gln Thr Arg Arg Phe Asn Glu Glu Leu Ala Gly Leu Asp Asn
50 55 60
Thr Val Val Leu Thr Val Ser Met Asp Leu Pro Phe Ala Gln Lys Arg
65 70 75 80
Trp Cys Gly Ala Glu Gly Leu Asp Asn Ala Ile Met Leu Ser Asp Tyr
85 90 95
Phe Asp His Ser Phe Gly Arg Asp Tyr Ala Leu Leu Ile Asn Glu Trp
100 105 110
His Leu Leu Ala Arg Ala Val Phe Val Leu Asp Thr Asp Asn Thr Ile
115 120 125
Arg Tyr Val Glu Tyr Val Asp Asn Ile Asn Ser Glu Pro Asn Phe Glu
130 135 140

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 724 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CCAGGCTGAT ACAAGTATCG CAGACATTCA AAAAAGAGGC GAACTGGTTG TCGGTGTCAA 60
ACAAGACGTT CCCAATTTTG GTTACAAnGA TCCAAGACC GGTACTTATT CTGGTATCGA 120
AaCCGACTTG GCCAAGATGG TAGCTGATGA ACTCAAGGTC AAGATTCGCT ATGTGCCGCT 180
TACAGCACAA ACCCGCGGCC CCCTTCTAGA CAATGAACAG GTCGATATGG ATATCGCGAC 240
CTTTACCATC ACGGACGAAC GCAAAAACT CTACAACTTT ACCAGTCCCT ACTACACAGA 300
CGCTTCTGGA TTTTGGTCA ATAAATCTGC CAAATCAAA AAGATTGAGG ACCTAAACGG 360
CAAAACCATC GGAGTCGCCC AAGGTTCTAT CACCCAACGC CTGATTACTG AACTGGGTAA 420

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AAAGAAAGGT CTGAAGTTTA AATTCGTCGA ACTTGGTTCC TACCCAGAAT TGATTACTTC      480
CCTGCACGCT CATCGTATCG ATACCTTTTC CGTTGACCGC TCTATTCTAT CTGGCTACAC      540
TAGTAAACGG ACAGCACTAC TAGATGATAG TTTCAAGCCA TCTGACTACG GTATTGTTAC      600
CAAGAAATCA AATACAGAGC TCAACGACTA TCTTGATAAC TTGGTTACTA AATGGAGCAA      660
GGATGGTAGT TTGCAGAAAC TTTATGACCG TTACAAGCTC AAACCATCTA GCCATACTGC      720
AGAT                                                                    724

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(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

a' cont.

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Gln Ala Asp Thr Ser Ile Ala Asp Ile Gln Lys Arg Gly Glu Leu Val
1           5           10          15
Val Gly Val Lys Gln Asp Val Pro Asn Phe Gly Tyr Xaa Asp Pro Lys
          20          25          30
Thr Gly Thr Tyr Ser Gly Ile Glu Thr Asp Leu Ala Lys Met Val Ala
          35          40          45
Asp Glu Leu Lys Val Lys Ile Arg Tyr Val Pro Val Thr Ala Gln Thr
          50          55          60
Arg Gly Pro Leu Leu Asp Asn Glu Gln Val Asp Met Asp Ile Ala Thr
          65          70          75          80
Phe Thr Ile Thr Asp Glu Arg Lys Lys Leu Tyr Asn Phe Thr Ser Pro
          85          90          95
Tyr Tyr Thr Asp Ala Ser Gly Phe Leu Val Asn Lys Ser Ala Lys Ile
          100          105          110
Lys Lys Ile Glu Asp Leu Asn Gly Lys Thr Ile Gly Val Ala Gln Gly
          115          120          125
Ser Ile Thr Gln Arg Leu Ile Thr Glu Leu Gly Lys Lys Lys Gly Leu
          130          135          140
Lys Phe Lys Phe Val Glu Leu Gly Ser Tyr Pro Glu Leu Ile Thr Ser
          145          150          155          160
Leu His Ala His Arg Ile Asp Thr Phe Ser Val Asp Arg Ser Ile Leu
          165          170          175
Ser Gly Tyr Thr Ser Lys Arg Thr Ala Leu Leu Asp Asp Ser Phe Lys
          180          185          190

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Pro Ser Asp Tyr Gly Ile Val Thr Lys Lys Ser Asn Thr Glu Leu Asn
 195 200 205

Asp Tyr Leu Asp Asn Leu Val Thr Lys Trp Ser Lys Asp Gly Ser Leu
 210 215 220

Gln Lys Leu Tyr Asp Arg Tyr Lys Leu Lys Pro Ser Ser His Thr Ala
 225 230 235 240

Asp

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GTCTGTATCA TTTGAAAACA AAGAAACAAA CCGTGGTGTG TTgACTTTCA CTATCTCTCA 60
 AGACCAAATC AAACCAGAAT TGGACCGTGT CTTCAAGtCA GTGAAGAAAT CTCTTAATGT 120
 TCCAGGTTTC CGTAAAGGTC ACCTTCCACG CCCTATCTTC GACC AAAAAT TTGGTGAAGA 180
 AGCTCTTTAT CAAGATGCAA TGAACGCACT TTTGCCAAAC GCTTATGAAG CAGCTGTAAA 240
 AGAAGCTGGT CTTGAAGTGG TTGCCCAACC AAAAATTGAC GTAAC TTCAA TGGAAAAAGG 300
 TCAAGACTGG GTTATCACTG CTGAAGTCGT TACAAAACCT GAAGTAAAAT TGGGTGACTA 360
 CAAAAACCTT GAAGTATCAG TTGATGTAGA AAAAGAAGTA ACTGACGCTG ATGTCGAAGA 420
 GCGTATCGAA CGCGAACGCA ACAACCTGGC TGAATTGGTT ATCAAGGAAG CTGCTGCTGA 480
 AAACGGCGAC ACTGTTGTGA TCGACTTCGT TGGTTCATC GACGGTGTG AATTTGACGG 540
 TGGAAAAGGT GAAACTTCT CACTTGGACT TGGTTCAGGT CAATTCATCC CTGGTTTCGA 600
 AGACCAATTG GTAGGTCAC TCGCTGGCGA AACCGTTGAT GTTATCGTAA CATTCACAGA 660
 AGACTACCAA GCAGAAGACC TTGCAGGTAA AGAAGCTAAA TTCGTGACAA CTATCCACGA 720
 AGTAAAAGCT AAAGAAGTTC CGGCTCTTGA CGATGAACTT GCAAAAGACA TTGATGAAGA 780
 AGTTGAAACA CTTGCTGACT TGAAAGAAAA ATACAGCAAA GAATTGGCTG CTGCTAAAGA 840
 AGAAGCTTAC AAAGATGCAG TTGAAGGTGC AGCAATTGAT ACAGCTGTAG AAAATGCTGA 900
 AATCGTAGAA CTTCCAGAAG AAATGATCCA TGAAGAAGTT CACCGTTCAG TAAATGAATT 960
 CCTTGGGAAT TTGCAACGTC AAGGGATCAA CCCTGACATG TACTTCCAAA TCACTGGAAC 1020
 TACTCAAGAA GACCTTCACA ACCAATACCA AGCAGAAGCT GAGTCACGTA CTAAGACTAA 1080
 CCTTGTTATC GAAGCAGTTG CCAAAGCTGA AGGATTTGAT GCTTCAGAAG AAGAAATCCA 1140
 AAAAGAAGTT GAGCAATTGG CAGCAGACTA CAACATGGAA GTTGCAACAAG TTCAAAACCT 1200

GCTTTCAGCT GACATGTTGA AACATGATAT CACTATCAAA AAAGCTGTTG AATTGATCAC 1260
 AAGCACAGCA ACAGTAAAA 1279

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser Val Ser Phe Glu Asn Lys Glu Thr Asn Arg Gly Val Leu Thr Phe
 1 5 10 15
 Thr Ile Ser Gln Asp Gln Ile Lys Pro Glu Leu Asp Arg Val Phe Lys
 20 25 30
 Ser Val Lys Lys Ser Leu Asn Val Pro Gly Phe Arg Lys Gly His Leu
 35 40 45
 Pro Arg Pro Ile Phe Asp Gln Lys Phe Gly Glu Glu Ala Leu Tyr Gln
 50 55 60
 Asp Ala Met Asn Ala Leu Leu Pro Asn Ala Tyr Glu Ala Ala Val Lys
 65 70 75 80
 Glu Ala Gly Leu Glu Val Val Ala Gln Pro Lys Ile Asp Val Thr Ser
 85 90 95
 Met Glu Lys Gly Gln Asp Trp Val Ile Thr Ala Glu Val Val Thr Lys
 100 105 110
 Pro Glu Val Lys Leu Gly Asp Tyr Lys Asn Leu Glu Val Ser Val Asp
 115 120 125
 Val Glu Lys Glu Val Thr Asp Ala Asp Val Glu Glu Arg Ile Glu Arg
 130 135 140
 Glu Arg Asn Asn Leu Ala Glu Leu Val Ile Lys Glu Ala Ala Ala Glu
 145 150 155 160
 Asn Gly Asp Thr Val Val Ile Asp Phe Val Gly Ser Ile Asp Gly Val
 165 170 175
 Glu Phe Asp Gly Gly Lys Gly Glu Asn Phe Ser Leu Gly Leu Gly Ser
 180 185 190
 Gly Gln Phe Ile Pro Gly Phe Glu Asp Gln Leu Val Gly His Ser Ala
 195 200 205
 Gly Glu Thr Val Asp Val Ile Val Thr Phe Pro Glu Asp Tyr Gln Ala
 210 215 220
 Glu Asp Leu Ala Gly Lys Glu Ala Lys Phe Val Thr Thr Ile His Glu

225 230 235 240
 Val Lys Ala Lys Glu Val Pro Ala Leu Asp Asp Glu Leu Ala Lys Asp
 245 250 255
 Ile Asp Glu Glu Val Glu Thr Leu Ala Asp Leu Lys Glu Lys Tyr Ser
 260 265 270
 Lys Glu Leu Ala Ala Ala Lys Glu Glu Ala Tyr Lys Asp Ala Val Glu
 275 280 285
 Gly Ala Ala Ile Asp Thr Ala Val Glu Asn Ala Glu Ile Val Glu Leu
 290 295 300
 Pro Glu Glu Met Ile His Glu Glu Val His Arg Ser Val Asn Glu Phe
 305 310 315 320
 Leu Gly Asn Leu Gln Arg Gln Gly Ile Asn Pro Asp Met Tyr Phe Gln
 325 330 335
 Ile Thr Gly Thr Thr Gln Glu Asp Leu His Asn Gln Tyr Gln Ala Glu
 340 345 350
 Ala Glu Ser Arg Thr Lys Thr Asn Leu Val Ile Glu Ala Val Ala Lys
 355 360 365
 Ala Glu Gly Phe Asp Ala Ser Glu Glu Glu Ile Gln Lys Glu Val Glu
 370 375 380
 Gln Leu Ala Ala Asp Tyr Asn Met Glu Val Ala Gln Val Gln Asn Leu
 385 390 395 400
 Leu Ser Ala Asp Met Leu Lys His Asp Ile Thr Ile Lys Lys Ala Val
 405 410 415
 Glu Leu Ile Thr Ser Thr Ala Thr Val Lys
 420 425

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 490 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

TGGTCAAAG GAAAGTCAGA CAGGAAAGGG GATGAAAATT GTGACCAGTT TTTATCCTAT	60
CTACGCTATG GTTAAGGAAG TATCTGGTGA CTTGAATGAT GTTCGGATGA TTCAGTCAAG	120
TAGTGGTATT CACTCCTTTG AACCTTCGGC AAATGATATC GCAGCCATCT ATGATGCAGA	180
TGTCTTTGTT TACCATTCTC ATACACTCGA ATCTTGGGCA GGAAGTCTGG ATCCAAATCT	240
AAAAAATCC AAAGTGAAGG TCTTAGAGGC TTCTGAGGGA ATGACCTTGG AACGTGTCCC	300
TGGACTAGAG GATGTGGAAG CAGGGGATGG AGTTGATGAA AAAACGCTCT ATGACCCTCA	360
CACATGGCTA GATCCTGAAA AAGCTGGAGA AGAAGCCCAA ATTATCGCTG ATAAACTTTC	420

AGAGGTGGAT AGTGAGCATA AAGAGACTTA TCAAAAAAAT GCGCAACCTT TATCAAAAAA

480

GCTCAGGAAT

490

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Gly Gln Lys Glu Ser Gln Thr Gly Lys Gly Met Lys Ile Val Thr Ser
1 5 10 15

Phe Tyr Pro Ile Tyr Ala Met Val Lys Glu Val Ser Gly Asp Leu Asn
20 25 30

Asp Val Arg Met Ile Gln Ser Ser Ser Gly Ile His Ser Phe Glu Pro
35 40 45

Ser Ala Asn Asp Ile Ala Ala Ile Tyr Asp Ala Asp Val Phe Val Tyr
50 55 60

His Ser His Thr Leu Glu Ser Trp Ala Gly Ser Leu Asp Pro Asn Leu
65 70 75 80

Lys Lys Ser Lys Val Lys Val Leu Glu Ala Ser Glu Gly Met Thr Leu
85 90 95

Glu Arg Val Pro Gly Leu Glu Asp Val Glu Ala Gly Asp Gly Val Asp
100 105 110

Glu Lys Thr Leu Tyr Asp Pro His Thr Trp Leu Asp Pro Glu Lys Ala
115 120 125

Gly Glu Glu Ala Gln Ile Ile Ala Asp Lys Leu Ser Glu Val Asp Ser
130 135 140

Glu His Lys Glu Thr Tyr Gln Lys Asn Ala Gln Pro Leu Ser Lys Lys
145 150 155 160

Leu Arg Asn

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1006 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GAAGGATAGA TATATTTTAG CATTTGAGAC ATCCTGTGAT GAGACCAGTG TCGCCGCTCTT 60
 GAAAAACGAC GATGAGCTCT TGTCCAATGT CATTGCTAGT CAAATTGAGA GTCACAAACG 120
 TTTTGGTGGC GTAGTGCCCG AAGTAGCCAG TCGTCACCAT GTCGAGGTCA TTACAGCCTG 180
 TATCGAGGAG GCATTGGCAG AAGCAGGGAT TACCGAAGAG GACGTGACAG CTGTTGCGGT 240
 TACCTACGGA CCAGGCTTGG TCGGAGCCTT GCTAGTTGGT TTGTCAAGCTG CCAAGGCCTT 300
 TGCTTGGGCT CACGGACTTC CACTGATTCC TGTTAATCAC ATGGCTGGGC ACCTCATGGC 360
 AGCTCAGAGT GTGAGCCTT TGGAGTTTCC CTTGCTAGCC CTCTTGGTCA GCGGCGGACA 420
 CACAGAGTTG GTTTATGTTT CGGAGGCAGG AGATTATAAG ATTGTTGGGG AAACCCGTGA 480
 TGATGCGGTT GGTGAGGCTT ATGATAAGGT CGGCCGTGTC ATGGGCTTGA CCTATCCTGC 540
 AGGTCGTGAG ATTGACGAGC TGGCTCATCA GGGCAGGAT ATTTATGATT TCCCCGTGC 600
 CATGATTAAG GAAGATAATC TGGAGTTCTC CTTCTCAGGT TTGAAATCTG CCTTTATCAA 660
 TCTTCATCAC AATGCCGAGC AAAAGGGAGA AAGCCTGTCT ACAGAAGATT TGTGTGCTTC 720
 CTTCCAAGCA GCAGTTATGG ACATTCTCAT GGCAAAAACC AAGAAGGCTT TGGAGAAATA 780
 TCCTGTTAAA ATCCTAGTTG TGGCAGGTGG TGTGGCAGCC AATAAAGGTC TCAGAGAACG 840
 CCTAGCAGCC GAAATCACAG ATGTCAAGGT TATCATCCCC CCTCTGCGAC TCTGCGGAGA 900
 CAATGCAGGT ATGATTGCCT ATGCCAGCGT CAGCNAGTGG AACAAAGAAA ACTTCGCAGG 960
 CTGGGACCTC AATGCCAAAC CAAGTCTTGC CTTTGATACC ATGGAA 1006

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Lys Asp Arg Tyr Ile Leu Ala Phe Glu Thr Ser Cys Asp Glu Thr Ser
 1 5 10 15
 Val Ala Val Leu Lys Asn Asp Asp Glu Leu Leu Ser Asn Val Ile Ala
 20 25 30
 Ser Gln Ile Glu Ser His Lys Arg Phe Gly Gly Val Val Pro Glu Val
 35 40 45
 Ala Ser Arg His His Val Glu Val Ile Thr Ala Cys Ile Glu Glu Ala
 50 55 60

Leu Ala Glu Ala Gly Ile Thr Glu Glu Asp Val Thr Ala Val Ala Val
 65 70 75 80
 Thr Tyr Gly Pro Gly Leu Val Gly Ala Leu Leu Val Gly Leu Ser Ala
 85 90 95
 Ala Lys Ala Phe Ala Trp Ala His Gly Leu Pro Leu Ile Pro Val Asn
 100 105 110
 His Met Ala Gly His Leu Met Ala Ala Gln Ser Val Glu Pro Leu Glu
 115 120 125
 Phe Pro Leu Leu Ala Leu Leu Val Ser Gly Gly His Thr Glu Leu Val
 130 135 140
 Tyr Val Ser Glu Ala Gly Asp Tyr Lys Ile Val Gly Glu Thr Arg Asp
 145 150 155 160
 Asp Ala Val Gly Glu Ala Tyr Asp Lys Val Gly Arg Val Met Gly Leu
 165 170 175
 Thr Tyr Pro Ala Gly Arg Glu Ile Asp Glu Leu Ala His Gln Gly Gln
 180 185 190
 Asp Ile Tyr Asp Phe Pro Arg Ala Met Ile Lys Glu Asp Asn Leu Glu
 195 200 205
 Phe Ser Phe Ser Gly Leu Lys Ser Ala Phe Ile Asn Leu His His Asn
 210 215 220
 Ala Glu Gln Lys Gly Glu Ser Leu Ser Thr Glu Asp Leu Cys Ala Ser
 225 230 235 240
 Phe Gln Ala Ala Val Met Asp Ile Leu Met Ala Lys Thr Lys Lys Ala
 245 250 255
 Leu Glu Lys Tyr Pro Val Lys Ile Leu Val Val Ala Gly Gly Val Ala
 260 265 270
 Ala Asn Lys Gly Leu Arg Glu Arg Leu Ala Ala Glu Ile Thr Asp Val
 275 280 285
 Lys Val Ile Ile Pro Pro Leu Arg Leu Cys Gly Asp Asn Ala Gly Met
 290 295 300
 Ile Ala Tyr Ala Ser Val Ser Xaa Trp Asn Lys Glu Asn Phe Ala Gly
 305 310 315 320
 Trp Asp Leu Asn Ala Lys Pro Ser Leu Ala Phe Asp Thr Met Glu
 325 330 335

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Key

GGTAGTTAAA GTTGGTATTA ACGGTTTCGG ACGTATCGGT CGTCTTGCTT TCCGTCGTAT 60
 CCAAAACGTA GAAGGTGTTG AAGTTACACG CATCAACGAC CTTACAGATC CAGTTATGCT 120
 TGCACACTTG TTGAAATACG ACACAACTCA AGGTCGTTTC GACGGTACTG TTGAAGTTAA 180
 AGAAGGTGGA TTTGAAGTTA ACGGTAAATT CATCAAAGTT TCTGCTGAAC GTGATCCAGA 240
 ACAAATCGAC TGGGCTACTG ACGGTGTAGA AATCGTTCTT GAAGCTACTG GTTCTTTTGC 300
 TAAGAAAGAA GCAGCTGAAA AACACCTTAA AGGTGGAGCT AAAAAAGTTG TTATCACTGC 360
 TCCTGGTGA AACGACGTTA AAACAGTTGT ATTCAACACT AACCACGACG TTCTTGACGG 420
 TACTGAAACA GTTATCTCAG GTGCTTCATG TACTACAAAC TGCTTGGCTC CAATGGCTAA 480
 AGCTCTTCAA GACAACTTTG GTGTTGTGA AGGATTGATG ACTACTATCC ACGCTTACAC 540
 TGGTGACCAA ATGATCCTTG ACGGACCACA CCGTGGTGGT GACCTTCGCC GTGCTCGCGC 600
 TGGTGCTGCA AACATCGTTC CTAACTCAAC TGGTGCTGCA AAAGCTATCG GTCTTGTAAT 660
 CCCAGAATTG AATGGTAAAC TTGACGGATC TGCACAACGC GTTCCAACTC CAACTGGATC 720
 AGTTACTGAA TTGGTAGCAG TTCTTGAAAA GAACGTTACT GTTGATGAAG TGAACGCAGC 780
 TATGAAAGCA GCTTCAAACG AATCATACGG TTACACAGAA GATCCAATCG TATCTTCAGA 840
 TATCGTAGGT ATGTCTTACG GTTCATTGTT TGACGCAACT CAAACTAAAG TTCTTGACGT 900
 TGACGGTAAA CAATTGGTTA AAGTTGTATC ATGGTACGAC AACGAAATGT CATACACTGC 960
 ACAACTTGTT CGTACTCTTG GAATACTTCG CAAAAATTGC 1000

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu Ala
 1 5 10 15
 Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile Asn
 20 25 30
 Asp Leu Thr Asp Pro Val Met Leu Ala His Leu Leu Lys Tyr Asp Thr
 35 40 45
 Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly Phe
 50 55 60
 Glu Val Asn Gly Lys Phe Ile Lys Val Ser Ala Glu Arg Asp Pro Glu
 65 70 75 80

Gln Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala Thr
 85 90 95
 Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu Lys Gly Gly
 100 105 110
 Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val Lys Thr
 115 120 125
 Val Val Phe Asn Thr Asn His Asp Val Leu Asp Gly Thr Glu Thr Val
 130 135 140
 Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met Ala Lys
 145 150 155 160
 Ala Leu Gln Asp Asn Phe Gly Val Val Glu Gly Leu Met Thr Thr Ile
 165 170 175
 His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His Arg Gly
 180 185 190
 Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val Pro Asn
 195 200 205
 Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu Leu Asn
 210 215 220
 Gly Lys Leu Asp Gly Ser Ala Gln Arg Val Pro Thr Pro Thr Gly Ser
 225 230 235 240
 Val Thr Glu Leu Val Ala Val Leu Glu Lys Asn Val Thr Val Asp Glu
 245 250 255
 Val Asn Ala Ala Met Lys Ala Ala Ser Asn Glu Ser Tyr Gly Tyr Thr
 260 265 270
 Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Met Ser Tyr Gly Ser
 275 280 285
 Leu Phe Asp Ala Thr Gln Thr Lys Val Leu Asp Val Asp Gly Lys Gln
 290 295 300
 Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr Thr Ala
 305 310 315 320
 Gln Leu Val Arg Thr Leu Gly Ile Leu Arg Lys Asn Cys
 325 330

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TTCTTACGAG TTGGGACTGT ATCAAGCTAG AACGGTTAAG GAAAATAATC GTGTTTCCTA

60

TATAGATGGA AAACAAGCGA CGCAAAAAAC GGAGAATTTG ACTCCTGATG AGGTTAGCAA	120
GCGTGAAGGA ATCAATGCTG AGCAAATCGT CATCAAGATA ACAGACCAAG GCTATGTCAC	180
TTACATGGC GACCACTATC ATTATTACAA TGGTAAGGTT CCTTATGACG CTATCATCAG	240
TGAAGAATTA CTCATGAAAG ATCCAAACTA TAAGCTAAAA GATGAGGATA TTGTTAATGA	300
GGTCAAGGGT GGATATGTTA TCAAGGTAGA TGGAAAATAC TATGTTTACC TTAAGGATGC	360
TGCCCACGCG GATAACGTCC GTACAAAAGA GGAAATCAAT CGACAAAAAC AAGAGCATAG	420
TCAACATCGT GAAGGTGGAA CTCCAAGAAA CGATGGTGCT GTTGCCTTGG CACGTTTCGA	480
AGGACGCTAT ACTACAGATG ATGGTTATAT CTTTAATGCT TCTGATATCA TAGAGGATAC	540
TGGTGATGCT TATATCGTTC CTCATGGAGA TCATTACCAT TACATTCCTA AGAATGAGTT	600
ATCAGCTAGC GAGTTGGCTG CTGCAGAAGC CTTCTATCTT GGTGAGGAA ATCTGTCAAA	660
TTCAAGAACC TATCGCCGAC AAAATAGCGA TAACACTTCA AGAACAACT GGGTACCTTC	720
TGTAAGCAAT CCAGGAACTA CAAATACTAA CACAAGCAAC AACAGCAACA CTAACAGTCA	780
AGCAAGTCAA AGTAATGACA TTGATAGTCT CTTGAAACAG CTCTACAAAC TGCCTTTGAG	840
TCAACGACAT GTAGAATCTG ATGGCCTTGT CTTTGATCCA GCACAAATCA CAAGTCGAAC	900
AGCTAGAGGT GTTGCAGTGC CACACGGAGA TCATTACCAC TTCATCCCTT ACTCTCAAAT	960
GTCTGAATTG GAAGAACGAA TCGCTCGTAT TATTCCCCTT CGTTATCGTT CAAACCATTG	1020
GGTACCAGAT TCAAGGCCAG AACAAACCAAG TCCACAACCG ACTCCGGAAC CTAGTCCAGG	1080
CCCGCAACCT GCACCAAATC TTAATAAGTA CTCAAATTCT TCTTTGGTTA GTCAGCTGGT	1140
ACGAAAAGTT GGGGAAGGAT ATGTATTCTA AGAAAAGGGC ATCTCTCGTT ATGTCTTTGC	1200
GAAAGATTTA CCATCTGAAA CTGTTAAAAA TCTTGAAAGC AAGTTATCAA AACAAAGAGAG	1260
TGTTTCACAC ACTTTAACTG CTAAAAAGA AAATGTTGCT CCTCGTGACC AAGAATTTTA	1320
TGATAAAGCA TATAATCTGT TAACTGAGGC TCATAAAGCC TTGTTTGNAA ATAAGGGTCG	1380
TAATTCTGAT TTCCAAGCCT TAGACAAATT ATTAGAACGC TTGAATGATG AATCGACTAA	1440
TAAAGAAAAA TTGGTAGATG ATTTATTGGC ATTCCTAGCA CCAATTACCC ATCCAGAGCG	1500
ACTTGGCAAA CCAAATTCCT AAATTGAGTA TACTGAAGAC GAAGTTCGTA TTGCTCAATT	1560
AGCTGATAAG TATACAACGT CAGATGGTTA CATTTTTGAT GAACATGATA TAATCAGTGA	1620
TGAAGGAGAT GCATATGTAA CGCCTCATAT GGGCCATAGT CACTGGATTG GAAAAGATAG	1680
CCTTTCTGAT AAGGAAAAAG TTGCAGCTCA AGCCTATACT AAAGAAAAAG GTATCCTACC	1740
TCCATCTCCA GACGCAGATG TTAAAGCAAA TCCAAGTGA GATAGTGCAG CAGCTATTTA	1800
CAATCGTGTG AAAGGGGAAA AACGAATTCC ACTCGTTCGA CTTCCATATA TGGTTGAGCA	1860
TACAGTTGAG GTTAAAAACG GTAATTTGAT TATTCCTCAT AAGGATCATT ACCATAATAT	1920
TAAATTTGCT TGGTTTGATG ATCACACATA CAAAGCTCCA AATGGCTATA CCTTGAAGA	1980

TTTGTTTGCG ACGATTAAGT ACTACGTAGA ACACCCTGAC GAACGTCCAC ATTCTAATGA 2040
 TGGATGGGGC AATGCCAGTG AGCATGTGTT AGGCAAGAAA GACCACAGTG AAGATCCAAA 2100
 TAAGAACTTC AAAGCGGATG AAGAGCCAGT AGAGGAAACA CCTGCTGAGC CAGAAGTCCC 2160
 TCAAGTAGAG ACTGAAAAAG TAGAAGCCCA ACTCAAAGAA GCAGAAGTTT TGCTTGCGAA 2220
 AGTAACGGAT TCTAGTCTGA AAGCCAATGC AACAGAAACT CTAGCTGGTT TACGAAATAA 2280
 TTTGACTCTT CAAATTATGG ATAACAATAG TATCATGGCA GAAGCAGAAA AATTACTTGC 2340
 GTTGTTAAAA GGAAGTAATC CTTTATCTGT AAGTAAGGAA AAAATAAAC 2389

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Tyr Glu Leu Gly Leu Tyr Gln Ala Arg Thr Val Lys Glu Asn Asn
 1 5 10 15
 Arg Val Ser Tyr Ile Asp Gly Lys Gln Ala Thr Gln Lys Thr Glu Asn
 20 25 30
 Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala Glu Gln
 35 40 45
 Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly Asp
 50 55 60
 His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile Ile Ser
 65 70 75 80
 Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Lys Leu Lys Asp Glu Asp
 85 90 95
 Ile Val Asn Glu Val Lys Gly Gly Tyr Val Ile Lys Val Asp Gly Lys
 100 105 110
 Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg Thr
 115 120 125
 Lys Glu Glu Ile Asn Arg Gln Lys Gln Glu His Ser Gln His Arg Glu
 130 135 140
 Gly Gly Thr Pro Arg Asn Asp Gly Ala Val Ala Leu Ala Arg Ser Gln
 145 150 155 160
 Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile
 165 170 175

Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp His Tyr
 180 185 190
 His Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala Ala Ala
 195 200 205
 Glu Ala Phe Leu Ser Gly Arg Gly Asn Leu Ser Asn Ser Arg Thr Tyr
 210 215 220
 Arg Arg Gln Asn Ser Asp Asn Thr Ser Arg Thr Asn Trp Val Pro Ser
 225 230 235 240
 Val Ser Asn Pro Gly Thr Thr Asn Thr Asn Thr Ser Asn Asn Ser Asn
 245 250 255
 Thr Asn Ser Gln Ala Ser Gln Ser Asn Asp Ile Asp Ser Leu Leu Lys
 260 265 270
 Gln Leu Tyr Lys Leu Pro Leu Ser Gln Arg His Val Glu Ser Asp Gly
 275 280 285
 Leu Val Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr Ala Arg Gly Val
 290 295 300
 Ala Val Pro His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Gln Met
 305 310 315 320
 Ser Glu Leu Glu Glu Arg Ile Ala Arg Ile Ile Pro Leu Arg Tyr Arg
 325 330 335
 Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln Pro Ser Pro Gln
 340 345 350
 Pro Thr Pro Glu Pro Ser Pro Gly Pro Gln Pro Ala Pro Asn Leu Lys
 355 360 365
 Ile Asp Ser Asn Ser Ser Leu Val Ser Gln Leu Val Arg Lys Val Gly
 370 375 380
 Glu Gly Tyr Val Phe Glu Glu Lys Gly Ile Ser Arg Tyr Val Phe Ala
 385 390 395 400
 Lys Asp Leu Pro Ser Glu Thr Val Lys Asn Leu Glu Ser Lys Leu Ser
 405 410 415
 Lys Gln Glu Ser Val Ser His Thr Leu Thr Ala Lys Lys Glu Asn Val
 420 425 430
 Ala Pro Arg Asp Gln Glu Phe Tyr Asp Lys Ala Tyr Asn Leu Leu Thr
 435 440 445
 Glu Ala His Lys Ala Leu Phe Xaa Asn Lys Gly Arg Asn Ser Asp Phe
 450 455 460
 Gln Ala Leu Asp Lys Leu Leu Glu Arg Leu Asn Asp Glu Ser Thr Asn
 465 470 475 480
 Lys Glu Lys Leu Val Asp Asp Leu Leu Ala Phe Leu Ala Pro Ile Thr
 485 490 495
 His Pro Glu Arg Leu Gly Lys Pro Asn Ser Gln Ile Glu Tyr Thr Glu
 500 505 510

Asp Glu Val Arg Ile Ala Gln Leu Ala Asp Lys Tyr Thr Thr Ser Asp
 515 520 525
 Gly Tyr Ile Phe Asp Glu His Asp Ile Ile Ser Asp Glu Gly Asp Ala
 530 535 540
 Tyr Val Thr Pro His Met Gly His Ser His Trp Ile Gly Lys Asp Ser
 545 550 555 560
 Leu Ser Asp Lys Glu Lys Val Ala Ala Gln Ala Tyr Thr Lys Glu Lys
 565 570 575
 Gly Ile Leu Pro Pro Ser Pro Asp Ala Asp Val Lys Ala Asn Pro Thr
 580 585 590
 Gly Asp Ser Ala Ala Ala Ile Tyr Asn Arg Val Lys Gly Glu Lys Arg
 595 600 605
 Ile Pro Leu Val Arg Leu Pro Tyr Met Val Glu His Thr Val Glu Val
 610 615 620
 Lys Asn Gly Asn Leu Ile Ile Pro His Lys Asp His Tyr His Asn Ile
 625 630 635 640
 Lys Phe Ala Trp Phe Asp Asp His Thr Tyr Lys Ala Pro Asn Gly Tyr
 645 650 655
 Thr Leu Glu Asp Leu Phe Ala Thr Ile Lys Tyr Tyr Val Glu His Pro
 660 665 670
 Asp Glu Arg Pro His Ser Asn Asp Gly Trp Gly Asn Ala Ser Glu His
 675 680 685
 Val Leu Gly Lys Lys Asp His Ser Glu Asp Pro Asn Lys Asn Phe Lys
 690 695 700
 Ala Asp Glu Glu Pro Val Glu Glu Thr Pro Ala Glu Pro Glu Val Pro
 705 710 715 720
 Gln Val Glu Thr Glu Lys Val Glu Ala Gln Leu Lys Glu Ala Glu Val
 725 730 735
 Leu Leu Ala Lys Val Thr Asp Ser Ser Leu Lys Ala Asn Ala Thr Glu
 740 745 750
 Thr Leu Ala Gly Leu Arg Asn Asn Leu Thr Leu Gln Ile Met Asp Asn
 755 760 765
 Asn Ser Ile Met Ala Glu Ala Glu Lys Leu Leu Ala Leu Leu Lys Gly
 770 775 780
 Ser Asn Pro Ser Ser Val Ser Lys Glu Lys Ile Asn
 785 790 795

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

TACTGAGATG CATCATAATC TAGGAGCTGA AAAGCGTTCA GCAGTGGCTA CTACTATCGA 60
 TAGTTTAAAG GAGCGAAGTC AAAAAGTCAG AGCACTATCT GATCCAAATG TGCGTTTTGT 120
 TCCCTTCTTT GGCTCTAGTG AATGGCTTCG TTTTGACGGT GCTCATCTCG CGGTATTAGC 180
 TGAGAAATAC AATCGTTTCCT ACCGTCCTTA TCTTTTAGGA CAGGGGGGAG CTGCATCGCT 240
 TAACCAATAT TTTGGAATGC AACAGATGTT ACCACAGCTG GAGAATAAAC AAGTTGTGTA 300
 TGTATCTCA CCTCAGTGGT TCAGTAAAAA TGGCTATGAT CCAGCAGCCT TCCAGCAGTA 360
 TTTAATGGA GACCAGTTGA CTAGTTTCTT GAAACATCAA TCTGGGGATC AGGCTAGTCA 420
 ATATGCAGCG ACTCGCTTAC TGCAACAGTT CCCAAACGTA GCTATGAAGG ACCTGGTTCA 480
 GAAGTTGGCA AGTAAAGAAG AATTGTCGAC AGCAGACAAT GAAATGATTG AATTATTGGC 540
 TCGTTTTAAT GAACGCCAAG CTTCC'TTTT TGGTCAGTTT TCGGTTAGAG GCTATGTTAA 600
 CTACGATAAG CATGTAGCTA AGTATTTAAA AATCTTGCCA GACCAGTTTT CTTATCAGGC 660
 AATAGAAGAT GTTGTCAAAG CAGATGCTGA AAAAAATACT TCCAATAATG AGATGGGAAT 720
 GGAAAATTAT TTCTATAATG AGCAGATCAA GAAGGATTTG AAGAAATTAA AGGATTCTCA 780
 GAAAAGCTTT ACCTATCTCA AGTCGCCAGA GTATAATGNN TTGCAGTTGG TTTTAACACA 840
 GTTTTCTAAA TCTAAGGTAA ACCCGATTTT TATCATTCCA CCTGTTAATA AAAAATGGAT 900
 GNACTATGCT GGTCTACGAG AGGATATGTA CCAACAAACG GTGCAGAAGA TTCGCTACCA 960
 GTTAGAAAGT CAAGGTTTTA CCAATATAGC AGATTTTTCT AAGGACGGCG GGGAGCCTTT 1020
 CTTTATGAAG GACACCATTC ACCTTGGTTG GTTGGGTTGG TTGGCTTTTG ACAAGGCAGT 1080
 TGATCCTTTC CTATCCAATC CCACACCAGC TCCGACTTAC CATCTGAATG AGCGCTTTTT 1140
 CAGCAAAGAT TGGGCGACTT ATGATGGAGA TGTCAAAGAA 1180

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Thr Glu Met His His Asn Leu Gly Ala Glu Lys Arg Ser Ala Val Ala
 1 5 10 15

Thr Thr Ile Asp Ser Phe Lys Glu Arg Ser Gln Lys Val Arg Ala Leu
 20 25 30

Ser Asp Pro Asn Val Arg Phe Val Pro Phe Phe Gly Ser Ser Glu Trp
 35 40 45
 Leu Arg Phe Asp Gly Ala His Ser Ala Val Leu Ala Glu Lys Tyr Asn
 50 55 60
 Arg Ser Tyr Arg Pro Tyr Leu Leu Gly Gln Gly Gly Ala Ala Ser Leu
 65 70 75 80
 Asn Gln Tyr Phe Gly Met Gln Gln Met Leu Pro Gln Leu Glu Asn Lys
 85 90 95
 Gln Val Val Tyr Val Ile Ser Pro Gln Trp Phe Ser Lys Asn Gly Tyr
 100 105 110
 Asp Pro Ala Ala Phe Gln Gln Tyr Phe Asn Gly Asp Gln Leu Thr Ser
 115 120 125
 Phe Leu Lys His Gln Ser Gly Asp Gln Ala Ser Gln Tyr Ala Ala Thr
 130 135 140
 Arg Leu Leu Gln Gln Phe Pro Asn Val Ala Met Lys Asp Leu Val Gln
 145 150 155 160
 Lys Leu Ala Ser Lys Glu Glu Leu Ser Thr Ala Asp Asn Glu Met Ile
 165 170 175
 Glu Leu Leu Ala Arg Phe Asn Glu Arg Gln Ala Ser Phe Phe Gly Gln
 180 185 190
 Phe Ser Val Arg Gly Tyr Val Asn Tyr Asp Lys His Val Ala Lys Tyr
 195 200 205
 Leu Lys Ile Leu Pro Asp Gln Phe Ser Tyr Gln Ala Ile Glu Asp Val
 210 215 220
 Val Lys Ala Asp Ala Glu Lys Asn Thr Ser Asn Asn Glu Met Gly Met
 225 230 235 240
 Glu Asn Tyr Phe Tyr Asn Glu Gln Ile Lys Lys Asp Leu Lys Lys Leu
 245 250 255
 Lys Asp Ser Gln Lys Ser Phe Thr Tyr Leu Lys Ser Pro Glu Tyr Asn
 260 265 270
 Xaa Leu Gln Leu Val Leu Thr Gln Phe Ser Lys Ser Lys Val Asn Pro
 275 280 285
 Ile Phe Ile Ile Pro Pro Val Asn Lys Lys Trp Met Xaa Tyr Ala Gly
 290 295 300
 Leu Arg Glu Asp Met Tyr Gln Gln Thr Val Gln Lys Ile Arg Tyr Gln
 305 310 315 320
 Leu Glu Ser Gln Gly Phe Thr Asn Ile Ala Asp Phe Ser Lys Asp Gly
 325 330 335
 Gly Glu Pro Phe Phe Met Lys Asp Thr Ile His Leu Gly Trp Leu Gly
 340 345 350
 Trp Leu Ala Phe Asp Lys Ala Val Asp Pro Phe Leu Ser Asn Pro Thr
 355 360 365

a'
 cont.

Pro Ala Pro Thr Tyr His Leu Asn Glu Arg Phe Phe Ser Lys Asp Trp
 370 375 380

Ala Thr Tyr Asp Gly Asp Val Lys Glu
 385 390

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1423 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GGTTTTGAGA AAGTATTTGC AGGGGGCCCT GATTGAGTCG ATTGAGCAAG TGGAAAATGA 60
 CCGTATTGTG GAAATTACAG TTTCCAATAA AAACGAGATT GGAGACCATA TCCAGGCTAC 120
 CTTGATTATC GAAATTATGG GGAAACACAG TAATATTCTA CTGGTCGATA AAAGCAGTCA 180
 TAAAATCCTC GAAGTTATCA AACACGTCGG CTTTTCACAA AATAGCTACC GCACCTTACT 240
 TCCAGGATCG ACCTATATCG CTCCGCCAAG TACAAAATCT CTCAATCCTT TTACTATCAA 300
 GGATGAAAAG CTCTTTGAAA TCCTGCAAAC CCAAGAACTA ACAGCAAAAA ATCTTCAAAG 360
 CCTCTTTCAA GGTCTGGGAC GCGATACGGC AAATGAATTG GAAAGGATAC TGCTTAGTGA 420
 AAAACTTTCC GCTTTCCGAA ATTTTTTCAA TCAAGAAACC AAGCCATGCT TGACTGAGAC 480
 TTCCTTCAGT CCAGTTCTTT TTGCAAATCA GGTGGGAGAG CCTTTTGCAA ATCTTTCTGA 540
 TTTGTTGGAC ACCTACTATA AGGATAAGGC TGAGCGCGAC CGCGTCAAAC AGCAGGCCAG 600
 TGAAGTGAAT CGTCGTGTTG AAAATGAACT TCAGAAAAAC CGACACAAAC TCAAAAAACA 660
 GGAAAAAGAG TTACTGGCGA CAGACAACGC TGAAGAATTT CGTCAAAAAG GAGAATTGCT 720
 GACAACCTTC CTCCACCAAG TGCCTAACGA CCAAGACCAG GTTATCCTAG ACAACTACTA 780
 TACCAACCAA CCTATCATGA TTGCGCTTGA TAAGGCTCTG ACTCCCAACC AGAATGCCCA 840
 ACGCTATTTT AAACGGTATC AGAAACTCAA AGAAGCTGTC AAATACITGA CTGATTTGAT 900
 TGAAGAAACC AAAGCCACTA TTCTCTATCT GGAAAGTGTA GAAACCGTCC TCAACCAAGC 960
 TGGACTGGAA GAAATCGCTG AAATCCGTGA AGAATTGATT CAAACAGGTT TTATCCGCAG 1020
 AAGACAACGG GAGAAAATCC AGAAACGCAA AAAACTAGAA CAATATCTAG CAAGCGATGG 1080
 CAAAACCATC ATCTATGTCG GACGAAACAA TCTTCAAAAT GAGGAATTGA CCTTTAAAAT 1140
 GGCCCGCAAG GAGGAACTTT GGTTCATGTC TAAGGACATT CCTGGAAGCC ATGTTGTCAT 1200
 CTCAGGAAAT CTTGACCCAT CTGATGCAGT CAAGACAGAC GCAGCAGAGT TAGCTGCCTA 1260
 CTTCTCTCAA GGGCGCCTGT CGAATCTGGT GCAGGTAGAT ATGATTGAAG TCAAAAAACT 1320

CAATAAACCA ACTGGTGGAA AACCCGGCTT TGTCACCTTAC ACAGGACAAA AGACCCTCCG 1380
 CGTCACACCA GACTCCAAAA AAATTGCATC CATGAAAAAA TCC 1423

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Val Leu Arg Lys Tyr Leu Gln Gly Ala Leu Ile Glu Ser Ile Glu Gln
 1 5 10 15
 Val Glu Asn Asp Arg Ile Val Glu Ile Thr Val Ser Asn Lys Asn Glu
 20 25 30
 Ile Gly Asp His Ile Gln Ala Thr Leu Ile Ile Glu Ile Met Gly Lys
 35 40 45
 His Ser Asn Ile Leu Leu Val Asp Lys Ser Ser His Lys Ile Leu Glu
 50 55 60
 Val Ile Lys His Val Gly Phe Ser Gln Asn Ser Tyr Arg Thr Leu Leu
 65 70 75 80
 Pro Gly Ser Thr Tyr Ile Ala Pro Pro Ser Thr Lys Ser Leu Asn Pro
 85 90 95
 Phe Thr Ile Lys Asp Glu Lys Leu Phe Glu Ile Leu Gln Thr Gln Glu
 100 105 110
 Leu Thr Ala Lys Asn Leu Gln Ser Leu Phe Gln Gly Leu Gly Arg Asp
 115 120 125
 Thr Ala Asn Glu Leu Glu Arg Ile Leu Val Ser Glu Lys Leu Ser Ala
 130 135 140
 Phe Arg Asn Phe Phe Asn Gln Glu Thr Lys Pro Cys Leu Thr Glu Thr
 145 150 155 160
 Ser Phe Ser Pro Val Pro Phe Ala Asn Gln Val Gly Glu Pro Phe Ala
 165 170 175
 Asn Leu Ser Asp Leu Leu Asp Thr Tyr Tyr Lys Asp Lys Ala Glu Arg
 180 185 190
 Asp Arg Val Lys Gln Gln Ala Ser Glu Leu Ile Arg Arg Val Glu Asn
 195 200 205
 Glu Leu Gln Lys Asn Arg His Lys Leu Lys Lys Gln Glu Lys Glu Leu
 210 215 220
 Leu Ala Thr Asp Asn Ala Glu Glu Phe Arg Gln Lys Gly Glu Leu Leu
 225 230 235 240

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cont

Thr Thr Phe Leu His Gln Val Pro Asn Asp Gln Asp Gln Val Ile Leu
 245 250 255
 Asp Asn Tyr Tyr Thr Asn Gln Pro Ile Met Ile Ala Leu Asp Lys Ala
 260 265 270
 Leu Thr Pro Asn Gln Asn Ala Gln Arg Tyr Phe Lys Arg Tyr Gln Lys
 275 280 285
 Leu Lys Glu Ala Val Lys Tyr Leu Thr Asp Leu Ile Glu Glu Thr Lys
 290 295 300
 Ala Thr Ile Leu Tyr Leu Glu Ser Val Glu Thr Val Leu Asn Gln Ala
 305 310 315 320
 Gly Leu Glu Glu Ile Ala Glu Ile Arg Glu Glu Leu Ile Gln Thr Gly
 325 330 335
 Phe Ile Arg Arg Arg Gln Arg Glu Lys Ile Gln Lys Arg Lys Lys Leu
 340 345 350
 Glu Gln Tyr Leu Ala Ser Asp Gly Lys Thr Ile Ile Tyr Val Gly Arg
 355 360 365
 Asn Asn Leu Gln Asn Glu Glu Leu Thr Phe Lys Met Ala Arg Lys Glu
 370 375 380
 Glu Leu Trp Phe His Ala Lys Asp Ile Pro Gly Ser His Val Val Ile
 385 390 395 400
 Ser Gly Asn Leu Asp Pro Ser Asp Ala Val Lys Thr Asp Ala Ala Glu
 405 410 415
 Leu Ala Ala Tyr Phe Ser Gln Gly Arg Leu Ser Asn Leu Val Gln Val
 420 425 430
 Asp Met Ile Glu Val Lys Lys Leu Asn Lys Pro Thr Gly Gly Lys Pro
 435 440 445
 Gly Phe Val Thr Tyr Thr Gly Gln Lys Thr Leu Arg Val Thr Pro Asp
 450 455 460
 Ser Lys Lys Ile Ala Ser Met Lys Lys Ser
 465 470

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GACAACATTT ACTATCCATA CAGTAGAGTC AGCACCAGCA GAAGTGAAAG AAATTCTTGA 60
 AACAGTAGAA AAAGACAACA ATGGCTATAT TCCCAACCTA ATCGGTCTCT TGGCCAATGC 120
 CCCGACTGTT TTAGAAGCCT ACCAAATGTG CTCATCTATC CACCGTCGCA ACAGCCTGAC 180

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ACCCGTTGAG CGTGAAGTGG TGCAAATCAC GGCAGCCGTG ACCAATGGTT GTGCCTTCTG 240
 TGTCGCAGGT CACACAGCCT TTTCCATCAA ACAAATCCAG ATGAATGATG ACTTGATTCA 300
 AGCTCTTCGC AATCGTACTC CAATTGAAAC AGATCCTAAA TTGGATACCC TAGCTAAGTT 360
 TACCTTGGCA GTTATCAATA CCAAGGGTCG TGTAGGAGAT GAAGCCTTGT CTGAGTTTTT 420
 AGAAGCTGGC TACACTCAAC AAAATGCCTT GGATGTGGTT TTTGGTGTCA GCCTAGCAAT 480
 CCTCTGTAAC TATGCCAACA ACTTAGCTAA TACACCAATT AATCCAGAAT TGCAACCTTA 540
 TGCC 544

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Thr Thr Phe Thr Ile His Thr Val Glu Ser Ala Pro Ala Glu Val Lys
 1 5 10 15
 Glu Ile Leu Glu Thr Val Glu Lys Asp Asn Asn Gly Tyr Ile Pro Asn
 20 25 30
 Leu Ile Gly Leu Leu Ala Asn Ala Pro Thr Val Leu Glu Ala Tyr Gln
 35 40 45
 Ile Val Ser Ser Ile His Arg Arg Asn Ser Leu Thr Pro Val Glu Arg
 50 55 60
 Glu Val Val Gln Ile Thr Ala Ala Val Thr Asn Gly Cys Ala Phe Cys
 65 70 75 80
 Val Ala Gly His Thr Ala Phe Ser Ile Lys Gln Ile Gln Met Asn Asp
 85 90 95
 Asp Leu Ile Gln Ala Leu Arg Asn Arg Thr Pro Ile Glu Thr Asp Pro
 100 105 110
 Lys Leu Asp Thr Leu Ala Lys Phe Thr Leu Ala Val Ile Asn Thr Lys
 115 120 125
 Gly Arg Val Gly Asp Glu Ala Leu Ser Glu Phe Leu Glu Ala Gly Tyr
 130 135 140
 Thr Gln Gln Asn Ala Leu Asp Val Val Phe Gly Val Ser Leu Ala Ile
 145 150 155 160
 Leu Cys Asn Tyr Ala Asn Asn Leu Ala Asn Thr Pro Ile Asn Pro Glu
 165 170 175

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cont.

Leu Gln Pro Tyr Ala
180

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 811 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GGCTAAGGAA AGAGTGGATG TACTAGCTTA TAAACAGGGG TTGTTTGAAA CGAGAGAGCA 60
 GGCCAAGCGA GGTGTGATGG CTGGCCTAGT CGTAGCAGTC CTTAATGGAG AACGGTTTGA 120
 CAAGCCAGGA GAGAAAATTC CAGATGACAC CGAATTAAAA CTCAAGGGGG AGAAACTCAA 180
 GTATGTCAGC CGTGGTGGTT TGAACTGGA AAAGGCCCTTG CAGGTCTTTG ATTTGTCGGT 240
 GGATGGCGCG ACTACGATTG ATATCGGGGC CTCTACTGGA GGTTTTACCG ATGTCATGCT 300
 ACAGAATAGT GCCAAGTTGG TCTTTGCAGT CGATGTTGGT ACCAATCAGT TGGCTTGGAA 360
 ATTACGCCAA GACCCACGAG TTGTCAGCAT GGAGCAGTTC AATTTCGCT ATGCTGAAAA 420
 GACTGATTTT GAGCAGGAGC CGAGCTTTGC CAGTATTGAT GTGAGTTTCA TTTCCCTTAG 480
 TCTGATTTTG CCAGCCTTGC ACCGTGTCTT GGCTGATCAA GGTCAGGTGG TAGCACTTGT 540
 CAAACCTCAG TTTGAGGCAG GACGTGAGCA GATTGGGAAA AATGGAATTA TTCGAGATGC 600
 TAAGGTTTCAT CAGAATGTCC TTGAATCTGT AACAGCTATG GCAGTAGAGG TAGGTTTTC 660
 AGTCCTTGGC TTGGACTTTT CTCCCATCCA AGGTGGACAT GGAAATATTG AATTTTTCAGC 720
 GTATTTGAAA AAAGAAAAGT CAGCAAGCAA TCAGATTCCTT GCTGAGATTA AAGAAGCAGT 780
 AGAGAGGGCG CATAGTCAAT TTAAAAATGA A 811

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 270 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ala Lys Glu Arg Val Asp Val Leu Ala Tyr Lys Gln Gly Leu Phe Glu
 1 5 10 15
 Thr Arg Glu Gln Ala Lys Arg Gly Val Met Ala Gly Leu Val Val Ala
 20 25 30

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Val Leu Asn Gly Glu Arg Phe Asp Lys Pro Gly Glu Lys Ile Pro Asp
 35 40 45
 Asp Thr Glu Leu Lys Leu Lys Gly Glu Lys Leu Lys Tyr Val Ser Arg
 50 55 60
 Gly Gly Leu Lys Leu Glu Lys Ala Leu Gln Val Phe Asp Leu Ser Val
 65 70 75 80
 Asp Gly Ala Thr Thr Ile Asp Ile Gly Ala Ser Thr Gly Gly Phe Thr
 85 90 95
 Asp Val Met Leu Gln Asn Ser Ala Lys Leu Val Phe Ala Val Asp Val
 100 105 110
 Gly Thr Asn Gln Leu Ala Trp Lys Leu Arg Gln Asp Pro Arg Val Val
 115 120 125
 Ser Met Glu Gln Phe Asn Phe Arg Tyr Ala Glu Lys Thr Asp Phe Glu
 130 135 140
 Gln Glu Pro Ser Phe Ala Ser Ile Asp Val Ser Phe Ile Ser Leu Ser
 145 150 155 160
 Leu Ile Leu Pro Ala Leu His Arg Val Leu Ala Asp Gln Gly Gln Val
 165 170 175
 Val Ala Leu Val Lys Pro Gln Phe Glu Ala Gly Arg Glu Gln Ile Gly
 180 185 190
 Lys Asn Gly Ile Ile Arg Asp Ala Lys Val His Gln Asn Val Leu Glu
 195 200 205
 Ser Val Thr Ala Met Ala Val Glu Val Gly Phe Ser Val Leu Gly Leu
 210 215 220
 Asp Phe Ser Pro Ile Gln Gly Gly His Gly Asn Ile Glu Phe Leu Ala
 225 230 235 240
 Tyr Leu Lys Lys Glu Lys Ser Ala Ser Asn Gln Ile Leu Ala Glu Ile
 245 250 255
 Lys Glu Ala Val Glu Arg Ala His Ser Gln Phe Lys Asn Glu
 260 265 270

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TTGTTCTAT GAAC TTGGTC GTCACCAAGC TGGTCAGGTT AAGAAAGAGT CTAATCGAGT 60
 TTCTTATATA GATGGTGATC AGGCTGGTCA AAAGGCAGAA AACTTGACAC CAGATGAAGT 120
 CAGTAAGAGG GAGGGGATCA ACGCCGAACA AATNGTNATC AAGATTACGG ATCAAGGTTA 180

TGTGACCTCT CATGGAGACC ATTATCATTA CTATAATGGC AAGGTTCCCTT ATGATGCCAT 240
 CATCAGTGAA GAGCTCCTCA TGAAAGATCC GAATTATCAG TTGAAGGATT CAGACATTGT 300
 CAATGAAATC AAGGGTGGTT ATGTCATTAA GGTAAACGGT AAATACTATG TNTACCTTAA 360
 GGATGCAGCT CATGCGGATA ATATTCCGAC AAAAGAAGAG ATTAAACGTC AGAAGCAGGA 420
 ACGCAGTCAT AATCATAACT CAAGAGCAGA TAATGCTGTT GCTGCAGCCA GAGCCCAAGG 480
 ACGTTATACA ACGGATGATG GGTATATCTT CAATGCATCT GATATCATTG AGGACACGGG 540
 TGATGCTTAT ATCGTTCCTC ACGGCGACCA TTACCATTAC ATTCCTAAGA ATGAGTTATC 600
 AGCTAGCGAG TTAGCTGCTG CAGAAGCCTA TTGGAATGGG AAGCAGGGAT CTCGTCCTTC 660
 TTCAAGTTCT AGTTATAATG CAAATCCAGC TCAACCAAGA TTGTCAGAGA ACCACAATCT 720
 GACTGTCACT CCAACTTATC ATCAAAATCA AGGGGAAAAC ATTTCAAGCC TTTTACGTGA 780
 ATGTATGCT AAACCCCTTAT CAGAACGCCA TGTGGAATCT GATGGCCTTA TTTTCGACCC 840
 AGCGCAAATC ACAAGTCGAA CCGCCAGAGG TGTAAGCTGTC CCTCATGGTA ACCATTACCA 900
 CTTTATCCCT TATGAACAAA TGTCTGAATT GGAAAAACGA ATTGCTCGTA TTATTCCCCT 960
 TCGTTATCGT TCAAACCATT GGGTACCAGA TTCAAGACCA GAACAACCAA GTCCACAATC 1020
 GACTCCGGAA CCTAGTCCAA GTCCGCAACC TGCACCAAT CCTCAACCAG CTCCAAGCAA 1080
 TCCAATTGAT GAGAAATTGG TCAAAGAAGC TGTTGAAAA GTAGGCGATG GTTATGTCTT 1140
 TGAGGAGAAT GGAGTTTCTC GTTATATCCC AGCCAAGGAT CTTTCAGCAG AACAGCAGC 1200
 AGGCATTGAT AGCAAACCTGG CCAAGCAGGA AAGTTTATCT CATAAGCTAG GAGCTAAGAA 1260
 AACTGACCTC CCATCTAGTG ATCGAGAATT TTACAATAAG GCTTATGACT TACTAGCAAG 1320
 AATTCACCAA GATTTACTTG ATAATAAAGG TCGACAAGTT GATTTTGAGG CTTTGGATAA 1380
 CCTGTTGGAA CGACTCAAGG ATGTCNCAAG TGATAAAGTC AAGTTAGTGG ANGATATTCT 1440
 TGCCTTCTTA GCTCCGATTG GTCATCCAGA ACGTTTAGGA AAACCAAATG CGCAAATTAC 1500
 CTACACTGAT GATGAGATTG AAGTAGCCAA GTTGGCAGGC AAGTACACAA CAGAAGACGG 1560
 TTATATCTTT GATCCTCGTG ATATAACCAG TGATGAGGGG GATGCCTATG TAACTCCACA 1620
 TATGACCCAT AGCCACTGGA TTAAAAAAGA TAGTTTGTCT GAAGCTGAGA GAGCGGCAGC 1680
 CCAGGCTTAT GCTAAAGAGA AAGGTTTGAC CCTCCTTCG ACAGACCATC AGGATTCAGG 1740
 AAATACTGAG GCAAAAGGAG CAGAAGCTAT CTACAACCGC GTGAAAGCAG CTAAGAAGGT 1800
 GCCACTGAT CGTATGCCTT ACAATCTTCA ATATACTGTA GAAGTCAAAA ACGGTAGTTT 1860
 AATCATACCT CATATGACC ATTACCATAA CATCAAAATT GAGTGGTTTG ACGAAGGCCT 1920
 TTATGAGGCA CCTAAGGGGT ATACTCTTGA GGATCTTTTG GCGACTGTCA AGTACTATGT 1980
 CGAACATCCA AACGAACGTC CGCATTCAGA TAATGGTTTT GGTAACGCTA GCGACCATGT 2040

TCAAAGAAAC AAAAATGGTC AAGCTGATAC CAATCAAACG GAAAAACCAA GCGAGGAGAA 2100
 ACCTCAGACA GAAAAACCTG AGGAAGAAAC CCCTCGAGAA GAGAAACCGC AAAGCGAGAA 2160
 ACCAGAGTCT CAAAAACCAA CAGAGGAACC AGAAGAATCA CCAGAGGAAT CAGAAGAACC 2220
 TCAGGTCGAG ACTGAAAAGG TTGAAGAAAA ACTGAGAGAG GCTGAAGATT TACTTGGAAG 2280
 AATCCAGGAT 2290

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Val Lys Lys Glu
 1 5 10 15
 Ser Asn Arg Val Ser Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala
 20 25 30
 Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala
 35 40 45
 Glu Gln Xaa Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His
 50 55 60
 Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile
 65 70 75 80
 Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp
 85 90 95
 Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys Val Asn
 100 105 110
 Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Ile
 115 120 125
 Arg Thr Lys Glu Glu Ile Lys Arg Gln Lys Gln Glu Arg Ser His Asn
 130 135 140
 His Asn Ser Arg Ala Asp Asn Ala Val Ala Ala Ala Arg Ala Gln Gly
 145 150 155 160
 Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile Ile
 165 170 175
 Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp His Tyr His
 180 185 190
 Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala Ala Ala Glu
 195 200 205

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Ala Tyr Trp Asn Gly Lys Gln Gly Ser Arg Pro Ser Ser Ser Ser Ser
 210 215 220
 Tyr Asn Ala Asn Pro Ala Gln Pro Arg Leu Ser Glu Asn His Asn Leu
 225 230 235 240
 Thr Val Thr Pro Thr Tyr His Gln Asn Gln Gly Glu Asn Ile Ser Ser
 245 250 255
 Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu Ser Glu Arg His Val Glu
 260 265 270
 Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr Ala
 275 280 285
 Arg Gly Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro Tyr
 290 295 300
 Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile Ile Pro Leu
 305 310 315 320
 Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln Pro
 325 330 335
 Ser Pro Gln Ser Thr Pro Glu Pro Ser Pro Ser Pro Gln Pro Ala Pro
 340 345 350
 Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val Lys
 355 360 365
 Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn Gly
 370 375 380
 Val Ser Arg Tyr Ile Pro Ala Lys Asp Leu Ser Ala Glu Thr Ala Ala
 385 390 395 400
 Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys Leu
 405 410 415
 Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr Asn
 420 425 430
 Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn
 435 440 445
 Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg
 450 455 460
 Leu Lys Asp Val Xaa Ser Asp Lys Val Lys Leu Val Xaa Asp Ile Leu
 465 470 475 480
 Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn
 485 490 495
 Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
 500 505 510
 Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile
 515 520 525
 Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser
 530 535 540

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cont.

His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala
 545 550 555 560
 Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His
 565 570 575
 Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn
 580 585 590
 Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn
 595 600 605
 Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His
 610 615 620
 Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu
 625 630 635 640
 Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val
 645 650 655
 Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly
 660 665 670
 Phe Gly Asn Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly Gln Ala
 675 680 685
 Asp Thr Asn Gln Thr Glu Lys Pro Ser Glu Glu Lys Pro Gln Thr Glu
 690 695 700
 Lys Pro Glu Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser Glu Lys
 705 710 715 720
 Pro Glu Ser Pro Lys Pro Thr Glu Glu Pro Glu Glu Ser Pro Glu Glu
 725 730 735
 Ser Glu Glu Pro Gln Val Glu Thr Glu Lys Val Glu Glu Lys Leu Arg
 740 745 750
 Glu Ala Glu Asp Leu Leu Gly Lys Ile Gln Asp
 755 760

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TTATAAGGGT GAATTAGAAA AAGGATACCA ATTTGATGGT TGGGAAATTT CTGGTTTCGA	60
AGGTAAAAAA GACGCTGGCT ATGTTATTAA TCTATCAAAA GATACCTTTA TAAAACCTGT	120
ATTCAAGAAA ATAGAGGAGA AAAAGGAGGA AGAAAATAAA CCTACTTTTG ATGTATCGAA	180
AAAGAAAGAT AACCCACAAG TAAACCATAG TCAATTAAAT GAAAGTCACA GAAAAGAGGA	240

TTTACAAAGA GAAGAGCATT CACAAAAATC TGATTCAACT AAGGATGTTA CAGCTACAGT 300
TCTTGATAAA AACAAATATCA GTAGTAAATC AACTACTAAC AATCCTAATA AG 352

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Tyr Lys Gly Glu Leu Glu Lys Gly Tyr Gln Phe Asp Gly Trp Glu Ile
1 5 10 15
Ser Gly Phe Glu Gly Lys Lys Asp Ala Gly Tyr Val Ile Asn Leu Ser
20 25 30
Lys Asp Thr Phe Ile Lys Pro Val Phe Lys Lys Ile Glu Glu Lys Lys
35 40 45
Glu Glu Glu Asn Lys Pro Thr Phe Asp Val Ser Lys Lys Lys Asp Asn
50 55 60
Pro Gln Val Asn His Ser Gln Leu Asn Glu Ser His Arg Lys Glu Asp
65 70 75 80
Leu Gln Arg Glu Glu His Ser Gln Lys Ser Asp Ser Thr Lys Asp Val
85 90 95
Thr Ala Thr Val Leu Asp Lys Asn Asn Ile Ser Ser Lys Ser Thr Thr
100 105 110
Asn Asn Pro Asn Lys
115

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GAATGTTTCAG GCTCAAGAAA GTTCAGGAAA TAAATCCAC TTTATCAATG TTCAAGAAGG 60
TGGCAGTGAT GCGATTATTC TTGAAAGCAA TGGACATTTT GCCATGGTGG ATACAGGAGA 120
AGATTATGAT TTCCAGATG GAAGTGATTC TCGCTATCCA TGGAGAGAAG GAATTGAAAC 180
GTCTTATAAG CATGTTCTAA CAGACCGTGT CTTTCGTCGT TTGAAGGAAT TGGGTGTCCA 240

AAAACTTGAT TTTATTTTGG TGACCCATAC CCACAGTGAT CATATTGGAA ATGTTGATGA 300
 ATTACTGTCT ACCTATCCAG TTGACCGAGT CTATCTTAAG AAATATAGTG ATAGTCGTAT 360
 TACTAATTCT GAACGTCTAT GGGATAATCT GTATGGCTAT GATAAGGTTT TACAGACTGC 420
 TGCAGAAAAA GGTGTTTCAG TTATTCAAAA TATCACACAA GGGGATGCTC ATTTTCAGTT 480
 TGGGGACATG GATATTTCAGC TCTATAATTA TGAAAATGAA ACTGATTCAT CGGGTGAATT 540
 AAAGAAAATT TGGGATGACA ATTCCAATTC CTTGATTAGC GTGGTGAAAG TCAATGGCAA 600
 GAAAATTTAC CTTGGGGGCG ATTTAGATAA TGTTTCATGGA GCAGAAGACA AGTATGGTCC 660
 TCTCATTTGA AAAGTTGATT TGATGAAGTT TAATCATCAC CATGATACCA ACAAATCAAA 720
 TACCAAGGAT TTCATTAAAA ATTTGAGTCC GAGTTTGATT GTTCAAACCT CGGATAGTCT 780
 ACCTTGGAAG AATGGTGTG ATAGTGAGTA TGTTAATTGG CTCAAAGAAC GAGGAATTGA 840
 GAGAATCAAC GCAGCCAGCA AAGACTATGA TGCAACAGTT TTTGATATTC GAAAAGACGG 900
 TTTTGTCAAT ATTTCAACAT CCTACAAGCC GATTCCAAGT TTTCAAGCTG GTTGGCATAA 960
 GAGTGCATAT GGGAACTGGT GGTATCAAGC GCCTGATTCT ACAGGAGAGT ATGCTGTCCG 1020
 TTGGAATGAA ATCGAAGGTG AATGGTATTA CTMTAACCAG ACGGGTATCT TGTTACAGAA 1080
 TCAATGGAAA AAATGGAACA ATCATTTGGT CTATTTGACA GACTCTGGTG CTCTGCTAA 1140
 AAATTGGAAG AAAATCGCTG GAATCTGGTA TTATTTTAAC AAAGAAAACC AGATGGAAAT 1200
 TGGTTGGATT CAAGATAAAG AGCAGTGGTA TTATTTGGAT GTTGATGGTT CTATGAAGAC 1260
 AGGATGGCTT CAATATATGG GGCAATGGTA TTACTIONTCT CCATCAGGGG AA 1312

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asn Val Gln Ala Gln Glu Ser Ser Gly Asn Lys Ile His Phe Ile Asn
 1 5 10 15
 Val Gln Glu Gly Gly Ser Asp Ala Ile Ile Leu Glu Ser Asn Gly His
 20 25 30
 Phe Ala Met Val Asp Thr Gly Glu Asp Tyr Asp Phe Pro Asp Gly Ser
 35 40 45
 Asp Ser Arg Tyr Pro Trp Arg Glu Gly Ile Glu Thr Ser Tyr Lys His
 50 55 60

Val Leu Thr Asp Arg Val Phe Arg Arg Leu Lys Glu Leu Gly Val Gln
 65 70 75 80
 Lys Leu Asp Phe Ile Leu Val Thr His Thr His Ser Asp His Ile Gly
 85 90 95
 Asn Val Asp Glu Leu Leu Ser Thr Tyr Pro Val Asp Arg Val Tyr Leu
 100 105 110
 Lys Lys Tyr Ser Asp Ser Arg Ile Thr Asn Ser Glu Arg Leu Trp Asp
 115 120 125
 Asn Leu Tyr Gly Tyr Asp Lys Val Leu Gln Thr Ala Ala Glu Lys Gly
 130 135 140
 Val Ser Val Ile Gln Asn Ile Thr Gln Gly Asp Ala His Phe Gln Phe
 145 150 155 160
 Gly Asp Met Asp Ile Gln Leu Tyr Asn Tyr Glu Asn Glu Thr Asp Ser
 165 170 175
 Ser Gly Glu Leu Lys Lys Ile Trp Asp Asp Asn Ser Asn Ser Leu Ile
 180 185 190
 Ser Val Val Lys Val Asn Gly Lys Lys Ile Tyr Leu Gly Gly Asp Leu
 195 200 205
 Asp Asn Val His Gly Ala Glu Asp Lys Tyr Gly Pro Leu Ile Gly Lys
 210 215 220
 Val Asp Leu Met Lys Phe Asn His His His Asp Thr Asn Lys Ser Asn
 225 230 235 240
 Thr Lys Asp Phe Ile Lys Asn Leu Ser Pro Ser Leu Ile Val Gln Thr
 245 250 255
 Ser Asp Ser Leu Pro Trp Lys Asn Gly Val Asp Ser Glu Tyr Val Asn
 260 265 270
 Trp Leu Lys Glu Arg Gly Ile Glu Arg Ile Asn Ala Ala Ser Lys Asp
 275 280 285
 Tyr Asp Ala Thr Val Phe Asp Ile Arg Lys Asp Gly Phe Val Asn Ile
 290 295 300
 Ser Thr Ser Tyr Lys Pro Ile Pro Ser Phe Gln Ala Gly Trp His Lys
 305 310 315 320
 Ser Ala Tyr Gly Asn Trp Trp Tyr Gln Ala Pro Asp Ser Thr Gly Glu
 325 330 335
 Tyr Ala Val Gly Trp Asn Glu Ile Glu Gly Glu Trp Tyr Tyr Phe Asn
 340 345 350
 Gln Thr Gly Ile Leu Leu Gln Asn Gln Trp Lys Lys Trp Asn Asn His
 355 360 365
 Trp Phe Tyr Leu Thr Asp Ser Gly Ala Ser Ala Lys Asn Trp Lys Lys
 370 375 380
 Ile Ala Gly Ile Trp Tyr Tyr Phe Asn Lys Glu Asn Gln Met Glu Ile
 385 390 395 400

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185

Gly Trp Ile Gln Asp Lys Glu Gln Trp Tyr Tyr Leu Asp Val Asp Gly
 405 410 415

Ser Met Lys Thr Gly Trp Leu Gln Tyr Met Gly Gln Trp Tyr Tyr Phe
 420 425 430

Ala Pro Ser Gly Glu
 435

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

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CTTGGGTGTA ACCCATATCC AGCTCCTTCC AGTCTTGTCT TACTACTTTG TCAATGAATT	60
GAAAAACCAT GAACGCTTGT CTGACTACGC TTCAAGCAAC AGCAACTACA ACTGGGGATA	120
TGACCCTCAA AACTACTTCT CCTTGACTGG TATGTACTCA AGCGATCCTA AGAATCCAGA	180
AAAACGAATC GCAGAATTTA AAAACCTCAT CAACGAAATC CACAAACGTG GTATGGGAGC	240
TATCCTAGAT GTCGTTTATA ACCACACAGC CAAAGTCGAT CTCTTTGAAG ATTTGGAACC	300
AAACTACTAC CACTTTATGG ATGCCGATGG CACACCTCGA ACTAGCTTTG GTGGTGGACG	360
CTTGGGGACA ACCCACCATA TGACCAAACG GCTCCTAATT GACTCTATCA AATACCTAGT	420
TGATACCTAC AAAGTGGATG GCTTCCGTTT CGATATGATG GGAGACCATG ACGCCGCTTC	480
TATCGAAGAA GCTTACAAGG CTGCACGCGC CCTCAATCCA AACCTCATCA TGCTTGGTGA	540
AGGTTGGAGA ACCTATGCCG GTGATGAAAA CATGCCTACT AAAGCTGCTG ACCAAGATTG	600
GATGAAACAT ACCGATACTG TCGCTGTCTT TTCAGATGAC ATCCGTAACA ACCTCAAATC	660
TGGTTATCCA AACGAAGGTC AACCTGCCTT TATCACAGGT GGCAAGCGTG ATGTCAACAC	720
CATCTTTAAA AATCTCATTT CTCAACCAAC TAACTTTGAA GCTGACAGCC CTGGAGATGT	780
CATCCAATAC ATCGCAGCCC ATGATAACTT GACCCTCTTT GACATCATTG CCCAGTCTAT	840
CAAAAAGAC CCAAGCAAGG CTGAGAACTA TGCTGAAATC CACCGTCGTT TACGACTTGG	900
AAATCTCATG GTCTTGACAG CTCAAGGAAC TCCATTTATC CACTCCGTC AGGAATATGG	960
ACGTACTAAA CAATTCCTG ACCCAGCCTA CAAGACTCCA GTAGCAGAGG ATAAGGTTCC	1020
AAACAAATCT CACTTGTTGC GTGATAAGGA CGGCAACCCA TTTGACTATC CTTACTTCAT	1080
CCATGACTCT TACGATTCTA GTGATGCAGT CAACAAGTTT GACTGGACTA AGGCTACAGA	1140
TGGTAAAGCT TATCCTGAAA ATGTCAAGAG CCGTGACTAT ATGAAAGGTT TGATTGCCCT	1200
TCGTCAATCT ACAGATGCCT TCCGACTTAA GAGTCTTCAA GATATCAAAG ACCGTGTCCA	1260

CCTCATCACT GTCCCAGGCC AAAATGGTGT GGAAAAAGAG GATGTAGTGA TTGGCTACCA 1320
 AATCACTGCT CCAAACGGCG ATATCTACGC AGTCTTTGTC AATGCGGATG AAAAAGCTCG 1380
 CGAATTTAAT TTGGGAACTG CCTTTGCACA TCTAAGAAAT GCGGAAGTTT TGGCAGATGA 1440
 AAACCAAGCA GGACCAGTCG GAATTGCCAA CCCGAAAGGA CTTGAATGGA CTGAAAAAGG 1500
 CTTGAAATTG AATGCCCTTA CAGCTACTGT TCTTCGAGTC TCTCAAAATG GAACTAGCCA 1560
 TGAGTCAACT GCAGAAGAGA AACCAGACTC AACCCCTTCC AAGCCTGAAC ATCAAAATGA 1620
 AGCTTCTCAC CCTGCACATC AAGACCCAGC TCCAGAAGCT AGACCTGATT CTACTAAACC 1680
 AGATGCCAAA GTAGCTGATG CGGAAAATAA ACCTAGCCAA GCTACAGCTG ATTCACAAGC 1740
 TGAACAACCA GCACAAGAAG CACAAGCATC ATCTGTAAAA GAAGCGGTTT GAAACGAATC 1800
 GGTAGAAAAC TCTAGCAAGG AAAATATACC TGCAACCCCA GATAACAAG CTGAA 1855

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Leu Gly Val Thr His Ile Gln Leu Leu Pro Val Leu Ser Tyr Tyr Phe
 1 5 10 15
 Val Asn Glu Leu Lys Asn His Glu Arg Leu Ser Asp Tyr Ala Ser Ser
 20 25 30
 Asn Ser Asn Tyr Asn Trp Gly Tyr Asp Pro Gln Asn Tyr Phe Ser Leu
 35 40 45
 Thr Gly Met Tyr Ser Ser Asp Pro Lys Asn Pro Glu Lys Arg Ile Ala
 50 55 60
 Glu Phe Lys Asn Leu Ile Asn Glu Ile His Lys Arg Gly Met Gly Ala
 65 70 75 80
 Ile Leu Asp Val Val Tyr Asn His Thr Ala Lys Val Asp Leu Phe Glu
 85 90 95
 Asp Leu Glu Pro Asn Tyr Tyr His Phe Met Asp Ala Asp Gly Thr Pro
 100 105 110
 Arg Thr Ser Phe Gly Gly Gly Arg Leu Gly Thr Thr His His Met Thr
 115 120 125
 Lys Arg Leu Leu Ile Asp Ser Ile Lys Tyr Leu Val Asp Thr Tyr Lys
 130 135 140
 Val Asp Gly Phe Arg Phe Asp Met Met Gly Asp His Asp Ala Ala Ser

145 150 155 160
 Ile Glu Glu Ala Tyr Lys Ala Ala Arg Ala Leu Asn Pro Asn Leu Ile
 165 170 175
 Met Leu Gly Glu Gly Trp Arg Thr Tyr Ala Gly Asp Glu Asn Met Pro
 180 185 190
 Thr Lys Ala Ala Asp Gln Asp Trp Met Lys His Thr Asp Thr Val Ala
 195 200 205
 Val Phe Ser Asp Asp Ile Arg Asn Asn Leu Lys Ser Gly Tyr Pro Asn
 210 215 220
 Glu Gly Gln Pro Ala Phe Ile Thr Gly Gly Lys Arg Asp Val Asn Thr
 225 230 235 240
 Ile Phe Lys Asn Leu Ile Ala Gln Pro Thr Asn Phe Glu Ala Asp Ser
 245 250 255
 Pro Gly Asp Val Ile Gln Tyr Ile Ala Ala His Asp Asn Leu Thr Leu
 260 265 270
 Phe Asp Ile Ile Ala Gln Ser Ile Lys Lys Asp Pro Ser Lys Ala Glu
 275 280 285
 Asn Tyr Ala Glu Ile His Arg Arg Leu Arg Leu Gly Asn Leu Met Val
 290 295 300
 Leu Thr Ala Gln Gly Thr Pro Phe Ile His Ser Gly Gln Glu Tyr Gly
 305 310 315 320
 Arg Thr Lys Gln Phe Arg Asp Pro Ala Tyr Lys Thr Pro Val Ala Glu
 325 330 335
 Asp Lys Val Pro Asn Lys Ser His Leu Leu Arg Asp Lys Asp Gly Asn
 340 345 350
 Pro Phe Asp Tyr Pro Tyr Phe Ile His Asp Ser Tyr Asp Ser Ser Asp
 355 360 365
 Ala Val Asn Lys Phe Asp Trp Thr Lys Ala Thr Asp Gly Lys Ala Tyr
 370 375 380
 Pro Glu Asn Val Lys Ser Arg Asp Tyr Met Lys Gly Leu Ile Ala Leu
 385 390 395 400
 Arg Gln Ser Thr Asp Ala Phe Arg Leu Lys Ser Leu Gln Asp Ile Lys
 405 410 415
 Asp Arg Val His Leu Ile Thr Val Pro Gly Gln Asn Gly Val Glu Lys
 420 425 430
 Glu Asp Val Val Ile Gly Tyr Gln Ile Thr Ala Pro Asn Gly Asp Ile
 435 440 445
 Tyr Ala Val Phe Val Asn Ala Asp Glu Lys Ala Arg Glu Phe Asn Leu
 450 455 460
 Gly Thr Ala Phe Ala His Leu Arg Asn Ala Glu Val Leu Ala Asp Glu
 465 470 475 480
 Asn Gln Ala Gly Pro Val Gly Ile Ala Asn Pro Lys Gly Leu Glu Trp

485	490	495
Thr Glu Lys Gly Leu Lys Leu Asn Ala Leu Thr Ala Thr Val Leu Arg 500	505	510
Val Ser Gln Asn Gly Thr Ser His Glu Ser Thr Ala Glu Glu Lys Pro 515	520	525
Asp Ser Thr Pro Ser Lys Pro Glu His Gln Asn Glu Ala Ser His Pro 530	535	540
Ala His Gln Asp Pro Ala Pro Glu Ala Arg Pro Asp Ser Thr Lys Pro 545	550	555
Asp Ala Lys Val Ala Asp Ala Glu Asn Lys Pro Ser Gln Ala Thr Ala 565	570	575
Asp Ser Gln Ala Glu Gln Pro Ala Gln Glu Ala Gln Ala Ser Ser Val 580	585	590
Lys Glu Ala Val Arg Asn Glu Ser Val Glu Asn Ser Ser Lys Glu Asn 595	600	605
Ile Pro Ala Thr Pro Asp Lys Gln Ala Glu 610	615	

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1774 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TAGTGATGGT ACTTGGCAAG GAAAACAGTA TCTGAAAGAA GATGGCAGTC AAGCAGCAAA 60
 TGAGTGGGTT TTNGATACTC ATTATCAATC TTGGTTCTAT ATAAAAGCAG ATGCTAACTA 120
 TGCTGAAAAT GAATGGCTAA AGCAAGGTGA CGACTATTTT TACCTCAAAT CTGGTGGCTA 180
 TATGGCCAAA TCAGAATGGG TAGAAGACAA GGGAGCCTTT TATTATCTTG ACCAAGATGG 240
 AAAGATGAAA AGAAATGCTT GGGTAGGAAC TTCCTATGTT GGTGCAACAG GTGCCAAAGT 300
 AATAGAAGAC TGGGTCTATG ATTCTCAATA CGATGCTTGG TTTTATATCA AAGCAGATGG 360
 ACAGCACGCA GAGAAAGAAT GGCTCCAAAT TAAAGGGAAG GACTATTATT TCAAATCCGG 420
 TGGTTATCTA CTGACAAGTC AGTGGATTAA TCAAGCTTAT GTGAATGCTA GTGGTGCCAA 480
 AGTACAGCAA GGTGGGCTTT TTGACAAACA ATACCAATCT TGGTTTACA TCAAAGAAAA 540
 TGGAACTAT GCTGATAAAG AATGGATTTT CGAGAATGGT CACTATTATT ATCTAAAATC 600
 CGGTGGCTAC ATGCGACCCA ATGAATGGAT TTGGGATAAG GAATCTTGGT TTTATCTCAA 660
 ATTTGATGGG AAAATGGCTG AAAAAGAATG GGTCTACGAT TCTCATAGTC AAGCTTGGTA 720
 CTAATTCAAA TCCGGTGGTT ACATGACAGC CAATGAATGG ATTTGGGATA AGGAATCTTG 780

GTTTTACCTC AAATCTGATG GGAAAATAGC TGAAAAAGAA TGGGTCTACG ATTCTCATAG 840
 TCAAGCTTGG TACTACTTCA AATCTGGTGG CTACATGGCG AAAAATGAGA CAGTAGATGG 900
 TTATCAGCTT GGAAGCGATG GTAAATGGCT TGGAGGAAAA ACTACAAATG AAAATGCTGC 960
 TTACTATCAA GTAGTGCCTG TTACAGCCAA TGTPTATGAT TCAGATGGTG AAAAGCTTTC 1020
 CTATATATCG CAAGGTAGTG TCGTATGGCT AGATAAGGAT AGAAAAAGTG ATGACAAGCG 1080
 CTGGCTATT ACTATTCTG GTTGTGTCAG CTATATGAAA ACAGAAGATT TACAAGCGCT 1140
 AGATGCTAGT AAGGACTTTA TCCCTTATTA TGAGAGTGAT GGCCACCGTT TTTATCACTA 1200
 TGTGGCTCAG AATGCTAGTA TCCAGTAGC TTCTCATCTT TCTGATATGG AAGTAGGCAA 1260
 GAAATATTAT TCGGCAGATG GCCTGCATTT TGATGGTTTT AAGCTTGAGA ATCCCTTCCT 1320
 TTTCAAAGAT TTAACAGAGG CTACAACTA CAGTGCTGAA GAATTGGATA AGGTATTTAG 1380
 TTTGCTAAAC ATTAACAATA GCCTTTTGGA GAACAAGGGC GCTACTTTTA AGGAAGCCGA 1440
 AGAACATTAC CATATCAATG CTCTTTATCT CCTTGCCCAT AGTGCCCTAG AAAGTAACTG 1500
 GGAAGAAGT AAAATTGCCA AAGATAAGAA TAATTCTTTT GGCATTACAG CCTATGATAC 1560
 GACCCCTTAC CTTTCTGCTA AGACATTTGA TGATGTGGAT AAGGGAATTT TAGGTGCAAC 1620
 CAAGTGGATT AAGGAAAATT ATATCGATAG GGAAGAAGT TTCCTTGGA ACAAGGCTTC 1680
 TGGTATGAAT GTGGAATATG CTTAGACCC TTATTGGGGC GAAAAAATG CTAGTGTGAT 1740
 GATGAAAATC AATGAGAAGC TAGGTGGCAA AGAT 1774

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 591 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ser Asp Gly Thr Trp Gln Gly Lys Gln Tyr Leu Lys Glu Asp Gly Ser
 1 5 10 15
 Gln Ala Ala Asn Glu Trp Val Xaa Asp Thr His Tyr Gln Ser Trp Phe
 20 25 30
 Tyr Ile Lys Ala Asp Ala Asn Tyr Ala Glu Asn Glu Trp Leu Lys Gln
 35 40 45
 Gly Asp Asp Tyr Phe Tyr Leu Lys Ser Gly Gly Tyr Met Ala Lys Ser
 50 55 60
 Glu Trp Val Glu Asp Lys Gly Ala Phe Tyr Tyr Leu Asp Gln Asp Gly

191

405	410	415
Glu Val Gly Lys Lys Tyr Tyr Ser Ala Asp Gly Leu His Phe Asp Gly 420 425 430		
Phe Lys Leu Glu Asn Pro Phe Leu Phe Lys Asp Leu Thr Glu Ala Thr 435 440 445		
Asn Tyr Ser Ala Glu Glu Leu Asp Lys Val Phe Ser Leu Leu Asn Ile 450 455 460		
Asn Asn Ser Leu Leu Glu Asn Lys Gly Ala Thr Phe Lys Glu Ala Glu 465 470 475 480		
Glu His Tyr His Ile Asn Ala Leu Tyr Leu Leu Ala His Ser Ala Leu 485 490 495		
Glu Ser Asn Trp Gly Arg Ser Lys Ile Ala Lys Asp Lys Asn Asn Phe 500 505 510		
Phe Gly Ile Thr Ala Tyr Asp Thr Thr Pro Tyr Leu Ser Ala Lys Thr 515 520 525		
Phe Asp Asp Val Asp Lys Gly Ile Leu Gly Ala Thr Lys Trp Ile Lys 530 535 540		
Glu Asn Tyr Ile Asp Arg Gly Arg Thr Phe Leu Gly Asn Lys Ala Ser 545 550 555 560		
Gly Met Asn Val Glu Tyr Ala Ser Asp Pro Tyr Trp Gly Glu Lys Ile 565 570 575		
Ala Ser Val Met Met Lys Ile Asn Glu Lys Leu Gly Gly Lys Asp 580 585 590		

(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

TGGGATTCAA TATGTCAGAG ATGATACTAG AGATAAAGAA GAGGGAATAG AGTATGATGA	60
CGCTGACAAT GGGGATATTA TTGTAAAAGT AGCGACTAAA CCTAAGGTAG TAACCAAGAA	120
AATTTCAACT ACGCGAATTC GTTATGAAAA AGATGAAACA AAAGACCGTA GTGAAAATCC	180
TGTTACAATT GATGGAGAGG ATGGCTATGT AACTACGACA AGGACCTACG ATGTTAATCC	240
AGAGACTGGT TATGTTACCG AACAGGTTAC TGTGATAGA AAAGAAGCCA CGGATACAGT	300
TATCAAAGTT CCAGCTAAAA GCAAGGTTGA AGAAGTTC TT GTTCCATTTG CTAATAAATA	360
TGAAGCAGAC AATGACCTTT CTGCAGGACA GGACGAAGAG ATTACTCTAG GAAAGAATGG	420
GAAAACAGTT ACAACGATAA CTTATAATGT AGATGGAAAG AGTGGACAAG TAACTGAGAG	480

TACTTTAAGT CAAAAAAG ACTCtCAAAC AAGAGTTGTT AAAAAAGaA CCArkCCCCA 540
 AGTTCTTGTC CAAGAAATTC CAATCGAAAC AGAATATCTC GATGGCCCaA CTCTTGATAA 600
 AaGTCAAGAA GTAGAAGAAG TAGGAGAAAT TGGTAAATTA CTCTTACTAC AATCTATACT 660
 GGTAGATGAA CGTGATGGAA CAATTGAAGA AACTACTTCT CGTCAAATTA CTAAAGAGAT 720
 GGTAAAAAGA CGTATAAGGA GAGGGACGAG AGAACCTGAA AAAGTTGTTG TTCCTGAGCA 780
 ATCATCTATT CCTTCGTATC CTGTATCTGT TACATCTAAC CAAGGAACAG ATGTAGCAGT 840
 AGAACCAGCT AAAGCAGTTG CTCCAACAAC AGACTGGAAA CAAGAAAATG GTATGTGGTA 900
 TTTTATAAT ACTGATGGTT CCATGGCAAC AGGTTGGGTA CAAGTTAATA GTTCATGGTA 960
 CTACCTCAAC AGCAACGGTT CTATGAAAGT CAATCAATGG TTCCAAGTTG GTGGTAAATG 1020
 GTATTATGTA AATACATCGG GTGAGTTAGC GGTCAATACA AGTATAGATG GCTATAGAGT 1080
 CAATGATAAT GGTGAATGGG TGCCT 1105

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Gly Ile Gln Tyr Val Arg Asp Asp Thr Arg Asp Lys Glu Glu Gly Ile
 1 5 10 15
 Glu Tyr Asp Asp Ala Asp Asn Gly Asp Ile Ile Val Lys Val Ala Thr
 20 25 30
 Lys Pro Lys Val Val Thr Lys Lys Ile Ser Ser Thr Arg Ile Arg Tyr
 35 40 45
 Glu Lys Asp Glu Thr Lys Asp Arg Ser Glu Asn Pro Val Thr Ile Asp
 50 55 60
 Gly Glu Asp Gly Tyr Val Thr Thr Thr Arg Thr Tyr Asp Val Asn Pro
 65 70 75 80
 Glu Thr Gly Tyr Val Thr Glu Gln Val Thr Val Asp Arg Lys Glu Ala
 85 90 95
 Thr Asp Thr Val Ile Lys Val Pro Ala Lys Ser Lys Val Glu Glu Val
 100 105 110
 Leu Val Pro Phe Ala Thr Lys Tyr Glu Ala Asp Asn Asp Leu Ser Ala
 115 120 125
 Gly Gln Glu Gln Glu Ile Thr Leu Gly Lys Asn Gly Lys Thr Val Thr
 130 135 140

Thr Ile Thr Tyr Asn Val Asp Gly Lys Ser Gly Gln Val Thr Glu Ser
 145 150 155 160
 Thr Leu Ser Gln Lys Lys Asp Ser Gln Thr Arg Val Val Lys Lys Arg
 165 170 175
 Thr Xaa Pro Gln Val Leu Val Gln Glu Ile Pro Ile Glu Thr Glu Tyr
 180 185 190
 Leu Asp Gly Pro Thr Leu Asp Lys Ser Gln Glu Val Glu Glu Val Gly
 195 200 205
 Glu Ile Gly Lys Leu Leu Leu Leu Gln Ser Ile Leu Val Asp Glu Arg
 210 215 220
 Asp Gly Thr Ile Glu Glu Thr Thr Ser Arg Gln Ile Thr Lys Glu Met
 225 230 235 240
 Val Lys Arg Arg Ile Arg Arg Gly Thr Arg Glu Pro Glu Lys Val Val
 245 250 255
 Val Pro Glu Gln Ser Ser Ile Pro Ser Tyr Pro Val Ser Val Thr Ser
 260 265 270
 Asn Gln Gly Thr Asp Val Ala Val Glu Pro Ala Lys Ala Val Ala Pro
 275 280 285
 Thr Thr Asp Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn Thr
 290 295 300
 Asp Gly Ser Met Ala Thr Gly Trp Val Gln Val Asn Ser Ser Trp Tyr
 305 310 315 320
 Tyr Leu Asn Ser Asn Gly Ser Met Lys Val Asn Gln Trp Phe Gln Val
 325 330 335
 Gly Gly Lys Trp Tyr Tyr Val Asn Thr Ser Gly Glu Leu Ala Val Asn
 340 345 350
 Thr Ser Ile Asp Gly Tyr Arg Val Asn Asp Asn Gly Glu Trp Val Arg
 355 360 365

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GGATAATAGA GAAGCATTAA AAACCTTTAT GACGGGTGAA AATTTTATC TCCAACATTA 60
 TCTAGGAGCA CATAGGGAAG AACTAAATGG AGAGCATGGC TATACCTTCC GTGTTTGGGC 120
 ACCTAATGCT CAGGCTGTTC ACTTGGTTGG TGATTTTACC AACTGGATTG AAAATCAGAT 180
 TCCAATGGTA AGAAATGATT TTGGGTCTG GGAAGTCTTT ACCAATATGG CTCAAGAAGG 240

GCATATTTAC AAATATCATG TCACACGTCA AAATGGTCAT CAACTGATGA AGATTGACCC 300
 TTTTGCTGTC AGGTATGAGG CTCGTCCAGG AACAGGGGCA ATCGTAACAG AGCTTCCTGA 360
 GAAGAAATGG AAGGATGGAC TTTGGCTGGC ACGAAGAAAA CGTTGGGGCT TTGAAGAGCG 420
 TCCTGTCAAT ATTTATGAAG TTCACGCTGG ATCATGGAAA AGAAATTCTG ATGGCAGTCC 480
 TTATAGTTTT GCCCAGCTCA AGGATGAACT CATTCCTTAT CTCGTTGAAA TGAACATAC 540
 TCATATTGAG TTTATGCCCT TGATGTCCCA TCCTTTGGGC TTGAGTTGGG GGTATCAGCT 600
 TATGGGTTAC TTCGCTTTAG AGCATGCTTA TGGCCGACCA GAGGAGTTTC AAGATTTTGT 660
 C 661

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 220 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Asp Asn Arg Glu Ala Leu Lys Thr Phe Met Thr Gly Glu Asn Phe Tyr
 1 5 10 15
 Leu Gln His Tyr Leu Gly Ala His Arg Glu Glu Leu Asn Gly Glu His
 20 25 30
 Gly Tyr Thr Phe Arg Val Trp Ala Pro Asn Ala Gln Ala Val His Leu
 35 40 45
 Val Gly Asp Phe Thr Asn Trp Ile Glu Asn Gln Ile Pro Met Val Arg
 50 55 60
 Asn Asp Phe Gly Val Trp Glu Val Phe Thr Asn Met Ala Gln Glu Gly
 65 70 75 80
 His Ile Tyr Lys Tyr His Val Thr Arg Gln Asn Gly His Gln Leu Met
 85 90 95
 Lys Ile Asp Pro Phe Ala Val Arg Tyr Glu Ala Arg Pro Gly Thr Gly
 100 105 110
 Ala Ile Val Thr Glu Leu Pro Glu Lys Lys Trp Lys Asp Gly Leu Trp
 115 120 125
 Leu Ala Arg Arg Lys Arg Trp Gly Phe Glu Glu Arg Pro Val Asn Ile
 130 135 140
 Tyr Glu Val His Ala Gly Ser Trp Lys Arg Asn Ser Asp Gly Ser Pro
 145 150 155 160
 Tyr Ser Phe Ala Gln Leu Lys Asp Glu Leu Ile Pro Tyr Leu Val Glu
 165 170 175

Met Asn Tyr Thr His Ile Glu Phe Met Pro Leu Met Ser His Pro Leu
 180 185 190

Gly Leu Ser Trp Gly Tyr Gln Leu Met Gly Tyr Phe Ala Leu Glu His
 195 200 205

Ala Tyr Gly Arg Pro Glu Glu Phe Gln Asp Phe Val
 210 215 220

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

AGATTTTGTC GAGGAGTGTC ATACCCATAA TATTGGGGTT ATTGTGGACT GGGTACCAGN 60
 TCACTTTACC ATCAACGATG ATGCCTTAGC CTATTATGAT GGGACACCGA CTTTGAATA 120
 CCAAGACCAT AATAAGGCTC ATAACCATGG TTGGGGTGCC CTTAATTTTG ACCTTGAAAA 180
 AAATGAAGTC CAGTCCTTCT TAATTTCTTG CATTAAGCAT TGGATTGATG TCTATCATTT 240
 GGATGGTATT CGTGTGGATG CTGTTAGCAA CATGCTCTAT TTGGACTATG ATGATGCTCC 300
 ATGGACACCT AATAAAGATG GCGGAAATCT CAACTATGAA GGTTATTATT TCCTTCAGCG 360
 CTTGAATGAG GTTATTAAGT TAGAATATCC AGATGTGATG ATGATTGCAG AAGAAAGTTC 420
 GTCTGCGATC AAGATTACGG GAATGAAAGA GATTGGTGGT CTAGGATTTG ACTACAAATG 480
 GAACATGGGC TGGATGAATG ATATCCTCCG TTTCTACGAA GAAGATCCGA TCTATCGTAA 540
 ATATGACTTT AACCTGGTGA CTTTCAGCTT TATGTATGTT TNCAAGGAGA ATTATCTCTT 600
 GCCATTCTCG CACGATGAAG TGGTTCATGG CAAGAAGAGT ATGATGCATA AGATGTGGGG 660
 AGATCGTTAC AATCAATTTC CAGGCTTGCG CAATCTCTAT ACGTACCAA TTTGTCACCC 720
 TGGTAAGAAA TTGCTCTTCA TGGGTAGCGA ATACGGTCAA TTCCTAGAAT GGAAATCTGA 780
 AGAACAGTTG GAATGGTCTA ACCTAGAAGA CCCAATGAAT GCTAAGATGA AGTATTTTCGC 840
 TTCTCAGCTA AACCAGTTTT ACAAGATCA TCGCTGTCTG TGGGAAATTG ATACCAGCTA 900
 TGATGGTATT GAAATCATTC ATGCGGATAA TCGAGACCAG AGTGTTCCTT CCTTTATTCG 960
 TAAGGGTAAA AAGGGA 976

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Asp Phe Val Glu Glu Cys His Thr His Asn Ile Gly Val Ile Val Asp
 1 5 10 15
 Trp Val Pro Xaa His Phe Thr Ile Asn Asp Asp Ala Leu Ala Tyr Tyr
 20 25 30
 Asp Gly Thr Pro Thr Phe Glu Tyr Gln Asp His Asn Lys Ala His Asn
 35 40 45
 His Gly Trp Gly Ala Leu Asn Phe Asp Leu Gly Lys Asn Glu Val Gln
 50 55 60
 Ser Phe Leu Ile Ser Cys Ile Lys His Trp Ile Asp Val Tyr His Leu
 65 70 75 80
 Asp Gly Ile Arg Val Asp Ala Val Ser Asn Met Leu Tyr Leu Asp Tyr
 85 90 95
 Asp Asp Ala Pro Trp Thr Pro Asn Lys Asp Gly Gly Asn Leu Asn Tyr
 100 105 110
 Glu Gly Tyr Tyr Phe Leu Gln Arg Leu Asn Glu Val Ile Lys Leu Glu
 115 120 125
 Tyr Pro Asp Val Met Met Ile Ala Glu Glu Ser Ser Ser Ala Ile Lys
 130 135 140
 Ile Thr Gly Met Lys Glu Ile Gly Gly Leu Gly Phe Asp Tyr Lys Trp
 145 150 155 160
 Asn Met Gly Trp Met Asn Asp Ile Leu Arg Phe Tyr Glu Glu Asp Pro
 165 170 175
 Ile Tyr Arg Lys Tyr Asp Phe Asn Leu Val Thr Phe Ser Phe Met Tyr
 180 185 190
 Val Xaa Lys Glu Asn Tyr Leu Leu Pro Phe Ser His Asp Glu Val Val
 195 200 205
 His Gly Lys Lys Ser Met Met His Lys Met Trp Gly Asp Arg Tyr Asn
 210 215 220
 Gln Phe Ala Gly Leu Arg Asn Leu Tyr Thr Tyr Gln Ile Cys His Pro
 225 230 235 240
 Gly Lys Lys Leu Leu Phe Met Gly Ser Glu Tyr Gly Gln Phe Leu Glu
 245 250 255
 Trp Lys Ser Glu Glu Gln Leu Glu Trp Ser Asn Leu Glu Asp Pro Met
 260 265 270
 Asn Ala Lys Met Lys Tyr Phe Ala Ser Gln Leu Asn Gln Phe Tyr Lys
 275 280 285
 Asp His Arg Cys Leu Trp Glu Ile Asp Thr Ser Tyr Asp Gly Ile Glu

290		295		300
Ile Ile Asp Ala Asp Asn Arg Asp Gln Ser Val Leu Ser Phe Ile Arg				
305		310		315 320
Lys Gly Lys Lys Gly				
		325		

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2134 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

a¹
cont.

ATCTGTAGTT TATGCGGATG AAACACTTAT TACTCATACT GCTGAGAAAC CTAAAGAGGA	60
AAAAATGATA GTAGAAGAAA AGGCTGATAA AGCTTTGGAA ACTAAAAATA TAGTTGAAAG	120
GACAGAACAA AGTGAACCTA GTTCAACTGA GGCTATTGCA TCTGAGNAGA AAGAAGATGA	180
AGCCGTAACCT CCAAAAAGAGG AAAAAGTGTC TGCTAAACCG GAAGAAAAAG CTCCAAGGAT	240
AGAATCACAA GCTTCAAATC AAGAAAAACC GCTCAAGGAA GATGCTAAAG CTGTAACAAA	300
TGAAGAAGTG AATCAAATGA TTGAAGACAG GAAAGTGGAT TTTAATCAAA ATTGGTACTT	360
TAAACTCAAT GCAAATCTTA AGGAAGCCAT TAAACCTGAT GCAGACGTAT CTACGTGGAA	420
AAAATTAGAT TTACCGTATG ACTGGAGTAT CTTTAACGAT TTCGATCATG AATCTCCTGC	480
ACAAAATGAA GGTGGACAGC TCAACGGTGG GGAAGCTTGG TATCGCAAGA CTTTCAAACCT	540
AGATGAAAAA GACCTCAAGA AAAATGTTTCG CCTTACTTTT GATGGCGTCT ACATGGATTTC	600
TCAAGTTTAT GTCAATGGTC AGTTAGTGGG GCATTATCCA AATGGTTATA ACCAGTTCTC	660
ATATGATATC ACCAAATACC TTCAAAAAGA TGGTCGTGAG AATGTGATTG CTGTCCATGC	720
AGTCAACAAA CAGCCAAGTA GCCGTTGGTA TTCAGGAAGT GGTATCTATC GTGATGTGAC	780
TTTACAAGTG ACAGATAAGG TGCATGTTGA GAAAAATGGG ACAACTATTT TAACACCAAA	840
ACTTGAAGAA CAACAACATG GCAAGGTTGA AACTCATGTG ACCAGCAAAA TCGTCAATAC	900
GGACGACAAA GACCATGAAC TTGTAGCCGA ATATCAAATC GTTGAACGAG GTGGTCATGC	960
TGTAACAGGC TTAGTTCGTA CAGCGAGTCG TACCTTAAAA GCACATGAAT CAACAAGCCT	1020
AGATGCGATT TTAGAAGTTG AAAGACCAAA ACTCTGGACT GTTTTAAATG ACAAACCTGC	1080
CTTGTACGAA TTGATTACGC GTGTTTACCG TGACGGTCAA TTGGTTGATG CTAAGAAGGA	1140
TTTGTTTGGT TACCGTTACT ATCACTGGAC TCCAAATGAA GGTTCCTCTT TGAATGGTGA	1200
ACGTATTAAA TTCCATGGAG TATCCTTGCA CCACGACCAT GGGGCGCTTG GAGCAGAAGA	1260
AAACTATAAA GCAGAATATC GCCGTCTCAA ACAAATGAAG GAGATGGGAG TTAACCTCAT	1320

CCGTACAACC CACAACCCTG CTAGTGAGCA AACCTTGCAA ATCGCAGCAG AACTAGGTTT 1380
 ACTCGTTCAG GAAGAGGCCT TTGATACGTG GTATGGTGGC AAGAAACCTT ATGACTATGG 1440
 ACGTTTCTTT GAAAAAGATG CCACTCACCC AGAAGCTCGA AAAGGTGAAA AATGGTCTGA 1500
 TTTTGACCTA CGTACCATGG TCGAAAGAGG CAAAAACAAC CCTGCTATCT TCATGTGGTC 1560
 AATTGGTAAT GAAATAGGTG AAGCTAATGG TGATGCCCAC TCTTTAGCAA CTGTTAAACG 1620
 TTTGGTTAAG GTTATCAAGG ATGTTGATAA GACTCGCTAT GTTACCATGG GAGCAGATAA 1680
 ATTCCGTTTC GGTAATGGTA GCGGAGGGCA TGAGAAAATT GCTGATGAAC TCGATGCTGT 1740
 TGGATTTAAC TATTCTGAAG ATAATTACAA AGCCCTTAGA GCTAAGCATC CAAAATGGTT 1800
 GATTTATGGA TCAGAAACAT CTTACAGTAC CCGTACACGT GGAAGTTACT ATCGCCCTGA 1860
 ACGTGAATTG AAACATAGCA ATGGACCTGA GCGTAATTAT GAACAGTCAG ATTATGGAAA 1920
 TGATCGTGTG GGTGGGGGA AAACAGCAAC CGCTTCATGG ACTTTTGACC GTGACAACGC 1980
 TGGCTATGCT GGACAGTTTA TCTGGACAGG TACGGACTAT ATTGGTGAAC CTACACCATG 2040
 GCACAACCAA AATCAAACCTC CTGTTAAGAG CTCTTACTTT GGTATCGTAG ATACAGCCGG 2100
 CATTCCAAAA CATGACTTCT ATCTCTACCA AAGC 2134

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 711 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ser Val Val Tyr Ala Asp Glu Thr Leu Ile Thr His Thr Ala Glu Lys
 1 5 10 15
 Pro Lys Glu Glu Lys Met Ile Val Glu Glu Lys Ala Asp Lys Ala Leu
 20 25 30
 Glu Thr Lys Asn Ile Val Glu Arg Thr Glu Gln Ser Glu Pro Ser Ser
 35 40 45
 Thr Glu Ala Ile Ala Ser Glu Xaa Lys Glu Asp Glu Ala Val Thr Pro
 50 55 60
 Lys Glu Glu Lys Val Ser Ala Lys Pro Glu Glu Lys Ala Pro Arg Ile
 65 70 75 80
 Glu Ser Gln Ala Ser Asn Gln Glu Lys Pro Leu Lys Glu Asp Ala Lys
 85 90 95
 Ala Val Thr Asn Glu Glu Val Asn Gln Met Ile Glu Asp Arg Lys Val

100 105 110
 Asp Phe Asn Gln Asn Trp Tyr Phe Lys Leu Asn Ala Asn Ser Lys Glu
 115 120 125
 Ala Ile Lys Pro Asp Ala Asp Val Ser Thr Trp Lys Lys Leu Asp Leu
 130 135 140
 Pro Tyr Asp Trp Ser Ile Phe Asn Asp Phe Asp His Glu Ser Pro Ala
 145 150 155 160
 Gln Asn Glu Gly Gly Gln Leu Asn Gly Gly Glu Ala Trp Tyr Arg Lys
 165 170 175
 Thr Phe Lys Leu Asp Glu Lys Asp Leu Lys Lys Asn Val Arg Leu Thr
 180 185 190
 Phe Asp Gly Val Tyr Met Asp Ser Gln Val Tyr Val Asn Gly Gln Leu
 195 200 205
 Val Gly His Tyr Pro Asn Gly Tyr Asn Gln Phe Ser Tyr Asp Ile Thr
 210 215 220
 Lys Tyr Leu Gln Lys Asp Gly Arg Glu Asn Val Ile Ala Val His Ala
 225 230 235 240
 Val Asn Lys Gln Pro Ser Ser Arg Trp Tyr Ser Gly Ser Gly Ile Tyr
 245 250 255
 Arg Asp Val Thr Leu Gln Val Thr Asp Lys Val His Val Glu Lys Asn
 260 265 270
 Gly Thr Thr Ile Leu Thr Pro Lys Leu Glu Glu Gln Gln His Gly Lys
 275 280 285
 Val Glu Thr His Val Thr Ser Lys Ile Val Asn Thr Asp Asp Lys Asp
 290 295 300
 His Glu Leu Val Ala Glu Tyr Gln Ile Val Glu Arg Gly Gly His Ala
 305 310 315 320
 Val Thr Gly Leu Val Arg Thr Ala Ser Arg Thr Leu Lys Ala His Glu
 325 330 335
 Ser Thr Ser Leu Asp Ala Ile Leu Glu Val Glu Arg Pro Lys Leu Trp
 340 345 350
 Thr Val Leu Asn Asp Lys Pro Ala Leu Tyr Glu Leu Ile Thr Arg Val
 355 360 365
 Tyr Arg Asp Gly Gln Leu Val Asp Ala Lys Lys Asp Leu Phe Gly Tyr
 370 375 380
 Arg Tyr Tyr His Trp Thr Pro Asn Glu Gly Phe Ser Leu Asn Gly Glu
 385 390 395 400
 Arg Ile Lys Phe His Gly Val Ser Leu His His Asp His Gly Ala Leu
 405 410 415
 Gly Ala Glu Glu Asn Tyr Lys Ala Glu Tyr Arg Arg Leu Lys Gln Met
 420 425 430
 Lys Glu Met Gly Val Asn Ser Ile Arg Thr Thr His Asn Pro Ala Ser

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435 440 445
 Glu Gln Thr Leu Gln Ile Ala Ala Glu Leu Gly Leu Leu Val Gln Glu
 450 455 460
 Glu Ala Phe Asp Thr Trp Tyr Gly Gly Lys Lys Pro Tyr Asp Tyr Gly
 465 470 475 480
 Arg Phe Phe Glu Lys Asp Ala Thr His Pro Glu Ala Arg Lys Gly Glu
 485 490 495
 Lys Trp Ser Asp Phe Asp Leu Arg Thr Met Val Glu Arg Gly Lys Asn
 500 505 510
 Asn Pro Ala Ile Phe Met Trp Ser Ile Gly Asn Glu Ile Gly Glu Ala
 515 520 525
 Asn Gly Asp Ala His Ser Leu Ala Thr Val Lys Arg Leu Val Lys Val
 530 535 540
 Ile Lys Asp Val Asp Lys Thr Arg Tyr Val Thr Met Gly Ala Asp Lys
 545 550 555 560
 Phe Arg Phe Gly Asn Gly Ser Gly Gly His Glu Lys Ile Ala Asp Glu
 565 570 575
 Leu Asp Ala Val Gly Phe Asn Tyr Ser Glu Asp Asn Tyr Lys Ala Leu
 580 585 590
 Arg Ala Lys His Pro Lys Trp Leu Ile Tyr Gly Ser Glu Thr Ser Ser
 595 600 605
 Ala Thr Arg Thr Arg Gly Ser Tyr Tyr Arg Pro Glu Arg Glu Leu Lys
 610 615 620
 His Ser Asn Gly Pro Glu Arg Asn Tyr Glu Gln Ser Asp Tyr Gly Asn
 625 630 635 640
 Asp Arg Val Gly Trp Gly Lys Thr Ala Thr Ala Ser Trp Thr Phe Asp
 645 650 655
 Arg Asp Asn Ala Gly Tyr Ala Gly Gln Phe Ile Trp Thr Gly Thr Asp
 660 665 670
 Tyr Ile Gly Glu Pro Thr Pro Trp His Asn Gln Asn Gln Thr Pro Val
 675 680 685
 Lys Ser Ser Tyr Phe Gly Ile Val Asp Thr Ala Gly Ile Pro Lys His
 690 695 700
 Asp Phe Tyr Leu Tyr Gln Ser
 705 710

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2167 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TTACTTTGGT ATCGTAGATA CAGCCGGCAT TCCAAAACAT GACTTC'TATC TCTACCAAAG 60
 CCAATGGGTT TCTGT'TAAGA AGAAACCGAT GGTACACCTT CTTCTCACT GGAAGTGGGA 120
 AAACAAAGAA TTAGCATCCA AAGTAGCTGA CTCAGAAGGT AAGATTCCAG TTCGTGCTTA 180
 TTCGAATGCT TCTAGTGTAG AATTGTTCTT GAATGGAAAA TCTCTTGGTC TTAAGACTTT 240
 CAATAAAAAA CAAACCAGCG ATGGGCGGAC TTACCAAGAA GTTGCAAATG CTAATGAAC'T 300
 TTATCTTGAA TGGAAAGTTG CCTATCAACC AGGTACCTTG GAAGCAATTG CTCGTGATGA 360
 ATCTGGCAAG GAAATTGCTC GAGATAAGAT TACGACTGCT GGTAAGCCAG CGGCAGTTCG 420
 TCTTATTAAG GAAGACCATG CGATTGCAGC AGATGGAAAA GACTTGACTT ACATCTACTA 480
 TGAAATTGTT GACAGCCAGG GGAATGTGGT TCCAAGTCTG AATAATCTGG TTCGCTTCCA 540
 ATTGCATGGC CAAGGTCAAC TGGTCGGTGT AGATAACGGA GAACAAGCCA GCCGTGAACG 600
 CTATAAGGCG CAAGCAGATG GTTCTTGGAT TCGTAAAGCA TTTAATGGTA AAGGTGTTGC 660
 CATTGTCAA TCAACTGAAC AAGCAGGGAA ATTCAACCTG ACTGCCCACT CTGATCTCTT 720
 GAAATCGAAC CAAGTCACTG TCTTTACTGG TAAGAAAGAA GGACAAGAGA AGACTGTTTT 780
 GGGGACAGAA GTGCCAAAAG TACAGACCAT TATTGGAGAG GCACCTGAAA TGCCTACCAC 840
 TGTTCCGTTT GTATACAGTG ATGGTAGCCG TGCAGAACGT CCTGTAACCT GGTCTTCAGT 900
 AGATGTGAGC AAGCCTGGTA TTGTAACGGT GAAAGGTATG GCTGACGGAC GAGAAGTAGA 960
 AGCTCGTGTA GAAGTGATTG CTCTTAAATC AGAGCTACCA GTTGTGAAAC GTATTGCTCC 1020
 AAATACTGAC TTGAATTCTG TAGACAAATC TGT'TTCCTAT GTTTTGATTG ATGGAAGTGT 1080
 TGAAGAGTAT GAAGTGGACA ACTGGGAGAT TGCCGAAGAA GATAAAGCTA AGTTAGCAAT 1140
 TCCAGGTTCT CGTATTCAAG CGACCGGTTA TTTAGAAGGT CAACCAATTC ATGCAACCCT 1200
 TGTGGTAGAA GAAGGCAATC CTGCGGCACC TGCAGTACCA ACTGTAACGG TTGGTGGTGA 1260
 GGCAGTAACA GGTCTTACTA GTCAAAAACC AATGCAATAC CGCACTCTTG CTTATGGAGC 1320
 TAAGTTGCCA GAAGTCACAG CAAGTGCTAA AAATGCAGCT GTTACAGTTC TTCAAGCAAG 1380
 CGCAGCAAAC GGCATGCGTG CGAGCATCTT TATT'CAGCCT AAAGATGGTG GCCCTCTTCA 1440
 AACCTATGCA ATTCAATTCC TTGAAGAAGC GCCAAAATTT GCTCACTTGA GCTTGCAAGT 1500
 GGAAAAAGCT GACAGTCTCA AAGAAGACCA AACTGTCAA TTGTCGGTTC GAGCTCACTA 1560
 TCAAGATGGA ACGCAAGCTG TATTACCAGC TGATAAAGTA ACCTTCTCTA CAAGTGGTGA 1620
 AGGGGAAGTC GCAATTGTA AAGGAATGCT TGAGTTGCAT AAGCCAGGAG CAGTCACTCT 1680
 GAACGCTGAA TATGAGGGAG CTAAAGACCA AGTTGAAC'TC ACTATCCAAG CCAATACTGA 1740
 GAAGAAGATT GCGCAATCCA TCCGTCCTGT AAATGTAGTG ACAGATTTGC ATCAGGAACC 1800
 AAGTCTTCCA GCAACAGTAA CAGTTGAGTA TGACAAAGGT TTCCCTAAAA CTCATAAAGT 1860

CACTTGGCAA GCTATTCCGA AAGAAAACT AGACTCCTAT CAAACATTTG AAGTACTAGG 1920
TAAAGTTGAA GGAATTGACC TTGAAGCGCG TGCAAAAGTC TCTGTAGAAG GTATCGTTTC 1980
AGTTGAAGAA GTCAGTGTGA CAACTCCAAT CGCAGAAGCA CCACAATTAC CAGAAAGTGT 2040
TCGGACATAT GATTCAAATG GTCACGTTTC ATCAGCTAAG GTTGCATGGG ATGCGATTTC 2100
TCCAGAGCAA TACGCTAAGG AAGGTGTCTT TACAGTTAAT GGTGCTTAG AAGGTACGCA 2160
ATTAACA 2167

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Tyr Phe Gly Ile Val Asp Thr Ala Gly Ile Pro Lys His Asp Phe Tyr
1 5 10 15
Leu Tyr Gln Ser Gln Trp Val Ser Val Lys Lys Lys Pro Met Val His
20 25 30
Leu Leu Pro His Trp Asn Trp Glu Asn Lys Glu Leu Ala Ser Lys Val
35 40 45
Ala Asp Ser Glu Gly Lys Ile Pro Val Arg Ala Tyr Ser Asn Ala Ser
50 55 60
Ser Val Glu Leu Phe Leu Asn Gly Lys Ser Leu Gly Leu Lys Thr Phe
65 70 75 80
Asn Lys Lys Gln Thr Ser Asp Gly Arg Thr Tyr Gln Glu Gly Ala Asn
85 90 95
Ala Asn Glu Leu Tyr Leu Glu Trp Lys Val Ala Tyr Gln Pro Gly Thr
100 105 110
Leu Glu Ala Ile Ala Arg Asp Glu Ser Gly Lys Glu Ile Ala Arg Asp
115 120 125
Lys Ile Thr Thr Ala Gly Lys Pro Ala Ala Val Arg Leu Ile Lys Glu
130 135 140
Asp His Ala Ile Ala Ala Asp Gly Lys Asp Leu Thr Tyr Ile Tyr Tyr
145 150 155 160
Glu Ile Val Asp Ser Gln Gly Asn Val Val Pro Thr Ala Asn Asn Leu
165 170 175
Val Arg Phe Gln Leu His Gly Gln Gly Gln Leu Val Gly Val Asp Asn
180 185 190

Gly Glu Gln Ala Ser Arg Glu Arg Tyr Lys Ala Gln Ala Asp Gly Ser
 195 200 205
 Trp Ile Arg Lys Ala Phe Asn Gly Lys Gly Val Ala Ile Val Lys Ser
 210 215 220
 Thr Glu Gln Ala Gly Lys Phe Thr Leu Thr Ala His Ser Asp Leu Leu
 225 230 235 240
 Lys Ser Asn Gln Val Thr Val Phe Thr Gly Lys Lys Glu Gly Gln Glu
 245 250 255
 Lys Thr Val Leu Gly Thr Glu Val Pro Lys Val Gln Thr Ile Ile Gly
 260 265 270
 Glu Ala Pro Glu Met Pro Thr Thr Val Pro Phe Val Tyr Ser Asp Gly
 275 280 285
 Ser Arg Ala Glu Arg Pro Val Thr Trp Ser Ser Val Asp Val Ser Lys
 290 295 300
 Pro Gly Ile Val Thr Val Lys Gly Met Ala Asp Gly Arg Glu Val Glu
 305 310 315 320
 Ala Arg Val Glu Val Ile Ala Leu Lys Ser Glu Leu Pro Val Val Lys
 325 330 335
 Arg Ile Ala Pro Asn Thr Asp Leu Asn Ser Val Asp Lys Ser Val Ser
 340 345 350
 Tyr Val Leu Ile Asp Gly Ser Val Glu Glu Tyr Glu Val Asp Lys Trp
 355 360 365
 Glu Ile Ala Glu Glu Asp Lys Ala Lys Leu Ala Ile Pro Gly Ser Arg
 370 375 380
 Ile Gln Ala Thr Gly Tyr Leu Glu Gly Gln Pro Ile His Ala Thr Leu
 385 390 395 400
 Val Val Glu Glu Gly Asn Pro Ala Ala Pro Ala Val Pro Thr Val Thr
 405 410 415
 Val Gly Gly Glu Ala Val Thr Gly Leu Thr Ser Gln Lys Pro Met Gln
 420 425 430
 Tyr Arg Thr Leu Ala Tyr Gly Ala Lys Leu Pro Glu Val Thr Ala Ser
 435 440 445
 Ala Lys Asn Ala Ala Val Thr Val Leu Gln Ala Ser Ala Ala Asn Gly
 450 455 460
 Met Arg Ala Ser Ile Phe Ile Gln Pro Lys Asp Gly Gly Pro Leu Gln
 465 470 475 480
 Thr Tyr Ala Ile Gln Phe Leu Glu Glu Ala Pro Lys Ile Ala His Leu
 485 490 495
 Ser Leu Gln Val Glu Lys Ala Asp Ser Leu Lys Glu Asp Gln Thr Val
 500 505 510
 Lys Leu Ser Val Arg Ala His Tyr Gln Asp Gly Thr Gln Ala Val Leu
 515 520 525

Pro Ala Asp Lys Val Thr Phe Ser Thr Ser Gly Glu Gly Glu Val Ala
 530 535 540
 Ile Arg Lys Gly Met Leu Glu Leu His Lys Pro Gly Ala Val Thr Leu
 545 550 555 560
 Asn Ala Glu Tyr Glu Gly Ala Lys Asp Gln Val Glu Leu Thr Ile Gln
 565 570 575
 Ala Asn Thr Glu Lys Lys Ile Ala Gln Ser Ile Arg Pro Val Asn Val
 580 585 590
 Val Thr Asp Leu His Gln Glu Pro Ser Leu Pro Ala Thr Val Thr Val
 595 600 605
 Glu Tyr Asp Lys Gly Phe Pro Lys Thr His Lys Val Thr Trp Gln Ala
 610 615 620
 Ile Pro Lys Glu Lys Leu Asp Ser Tyr Gln Thr Phe Glu Val Leu Gly
 625 630 635 640
 Lys Val Glu Gly Ile Asp Leu Glu Ala Arg Ala Lys Val Ser Val Glu
 645 650 655
 Gly Ile Val Ser Val Glu Glu Val Ser Val Thr Thr Pro Ile Ala Glu
 660 665 670
 Ala Pro Gln Leu Pro Glu Ser Val Arg Thr Tyr Asp Ser Asn Gly His
 675 680 685
 Val Ser Ser Ala Lys Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr
 690 695 700
 Ala Lys Glu Gly Val Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln
 705 710 715 720
 Leu Thr

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

AGCTAAGGTT GCATGGGATG CGATTTCGTCC AGAGCAATAC GCTAAGGAAG GTGTCTTTAC 60
 AGTTAATGGT CGCTTAGAAG GTACGCAATT AACAACTAAA CTTTCATGTTT GCGTATCTGC 120
 TCAAACGTAG CAAGGTGCAA ACATTTCTGA CCAATGGACC GGTTCAGAAT TGCCACTTGC 180
 CTTTGCTTCA GACTCAAATC CAAGCGACCC AGTTTCAAAT GTTAATGACA AGCTCATTTT 240
 CTACAATAAC CAACCAGCCA ATCGTTGGAC AAAGTGAAT CGTACTAATC CAGAAGCTTC 300
 AGTCGGTGTT CTGTTTGGAG ATTCAGGTAT CTTGAGCAAA CGCTCCGTTG ATAATCTAAG 360

TGTCGGATTC CATGAAGACC ATGGAGTTGG TGTACCGAAG TCTTATGTGA TTGAGTATTA 420
 TGTGTGTAAG ACTGTCCCAA CAGCTCCTAA AAACCCTAGT TTTGTGGTA ATGAGGACCA 480
 TGTCTTTAAT GATTCTGCCA ACTGGAAACC AGTTACTAAT CTAAAAGCCC CTGCTCAACT 540
 CAAGGCTGGA GAAATGAACC ACTTTAGCTT TGATAAAGTT GAAACCTATG CTGTTCTGAT 600
 TCGCATGGTT AAAGCAGATA ACAAGCGTGG AACGTCTATC ACAGAGGTAC AAATCTTTGC 660
 GAAACAAGTT GCGGCAGCCA AGCAAGGACA AACAAGAATC CAAGTTGACG GCAAAGACTT 720
 AGCAAACCTC AACCTGATT TGACAGACTA CTACCTTGAG TCTGTAGATG GAAAAGTTCC 780
 GGCAGTCACA GCAAGTGTTA GCAACAATGG TCTCGCTACC GTCGTTCCAA GCGTTCGTGA 840
 AGGTGAGCCA GTTCGTGTCA TCGCGAAAGC TGAAAATGGC GACATCTTAG GAGAATACCG 900
 TCTGCACTTC ACTAAGGATA AGAGCTTACT TTCTCATAAA CCAGTTGCTG CCGTTAAACA 960
 AGCTCGCTTG CTACAAGTAG GTCAAGCACT TGAATTGCCG ACTAAGGTC CAGTTTACTT 1020
 CACAGGTAAA GACGGCTACG AAACAAAAGA CCTGACAGTT GAATGGGAAG AAGTTCCAGC 1080
 GGAAAATCTG ACAAAGCAG GTCAATTTAC TGTTCGAGGC CGTGTCTTTG GTAGTAACCT 1140
 TGTGCTGAG ATCACTGTAC GAGTGACAGA CAACTTGGT GAGACTCTTT CAGATAACCC 1200
 TAACTATGAT GAAAACAGTA ACCAGGCCTT TGCTTCAGCA ACCAATGATA TTGACAAAAA 1260
 CTCTCATGAC CGCGTTGACT ATCTCAATGA CGGAGATCAT TCAGAAAATC GTCGTTGGAC 1320
 AAAGTGGTCA CCAACACCAT CTCTAATCC AGAAGTATCA GCGGGTGTGA TTTTCCGTGA 1380
 AAATGGTAAG ATTGTAGAAC GGAAGTGTAC ACAAGGAAAA GTTCAGTTCT TTGCAGATAG 1440
 TGGTACGGAT GCACCATCTA AACTCGTTT AGAACGCTAT GTCGGTCCAG AGTTTGAAGT 1500
 GCCAACCTAC TATTCAAACCT ACCAAGCCTA CGACGCAGAC CATCCATTCA ACAATCCAGA 1560
 AAATTTGGGAA GCTGTTCTTT ATCGTGCGGA TAAAGACATT GCAGCTGGTG ATGAAATCAA 1620
 CGTAACATTT AAAGCTATCA AAGCCAAAGC TATGAGATGG CGTATGGAGC GTAAAGCAGA 1680
 TAAGAGCGGT GTTGCATGA TTGAGATGAC CTTCTTTGCA CCAAGTGAAT TGCCTCAAGA 1740
 AAGCACTCAA TCAAAGATTC TTGTAGATGG AAAAGAACTT GCTGATTTG CTGAAAATCG 1800
 TCAAGACTAT CAAATTACCT ATAAAGGTCA ACGGCCAAAA GTCTCAGTTG AAGAAAACAA 1860
 TCAAGTAGCT TCAACTGTGG TAGATAGTGG AGAAGATAGC TTTCCAGTAC TTGTTCCGCT 1920
 CGTTTCAGAA AGTGAAAAC AAGTCAAGGA ATACCGTATC CACTTGACTA AGGAAAAC 1980
 AGTTTCTGAG AAGACAGTTG CTGCTGTACA AGAAGATCTT CCAAAAATCG AATTTGTTGA 2040
 AAAAGATTTG GCATACAAGA CAGTTGAGAA AAAAGATTCA AACTGTATC TAGGTGAAAC 2100
 TCGTGTAGAA CAAGAAGGAA AAGTTGGAAA AGAACGTATC TTTACAGCGA TTAATCCTGA 2160
 TGGAAGTAAG GAAGAAAAAC TCCGTGAAGT GGTAGAAGTT CCGACAGACC GCATCGTCTT 2220

GGTTGGAACC AAACCACTAG CTCAAGAAGC TAAAAAACCA CAAGTGTCTAG AAAAAGCAGA 2280
TACAAAACCA ATTGATTCAA GTGAAGCTAG TCAAATAAT AAAGCCCAG 2329

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Ala Lys Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr Ala Lys Glu
1 5 10 15
Gly Val Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln Leu Thr Thr
20 25 30
Lys Leu His Val Arg Val Ser Ala Gln Thr Glu Gln Gly Ala Asn Ile
35 40 45
Ser Asp Gln Trp Thr Gly Ser Glu Leu Pro Leu Ala Phe Ala Ser Asp
50 55 60
Ser Asn Pro Ser Asp Pro Val Ser Asn Val Asn Asp Lys Leu Ile Ser
65 70 75 80
Tyr Asn Asn Gln Pro Ala Asn Arg Trp Thr Asn Trp Asn Arg Thr Asn
85 90 95
Pro Glu Ala Ser Val Gly Val Leu Phe Gly Asp Ser Gly Ile Leu Ser
100 105 110
Lys Arg Ser Val Asp Asn Leu Ser Val Gly Phe His Glu Asp His Gly
115 120 125
Val Gly Val Pro Lys Ser Tyr Val Ile Glu Tyr Tyr Val Gly Lys Thr
130 135 140
Val Pro Thr Ala Pro Lys Asn Pro Ser Phe Val Gly Asn Glu Asp His
145 150 155 160
Val Phe Asn Asp Ser Ala Asn Trp Lys Pro Val Thr Asn Leu Lys Ala
165 170 175
Pro Ala Gln Leu Lys Ala Gly Glu Met Asn His Phe Ser Phe Asp Lys
180 185 190
Val Glu Thr Tyr Ala Val Arg Ile Arg Met Val Lys Ala Asp Asn Lys
195 200 205
Arg Gly Thr Ser Ile Thr Glu Val Gln Ile Phe Ala Lys Gln Val Ala
210 215 220
Ala Ala Lys Gln Gly Gln Thr Arg Ile Gln Val Asp Gly Lys Asp Leu
225 230 235 240

Ala Asn Phe Asn Pro Asp Leu Thr Asp Tyr Tyr Leu Glu Ser Val Asp
 245 250 255
 Gly Lys Val Pro Ala Val Thr Ala Ser Val Ser Asn Asn Gly Leu Ala
 260 265 270
 Thr Val Val Pro Ser Val Arg Glu Gly Glu Pro Val Arg Val Ile Ala
 275 280 285
 Lys Ala Glu Asn Gly Asp Ile Leu Gly Glu Tyr Arg Leu His Phe Thr
 290 295 300
 Lys Asp Lys Ser Leu Leu Ser His Lys Pro Val Ala Ala Val Lys Gln
 305 310 315 320
 Ala Arg Leu Leu Gln Val Gly Gln Ala Leu Glu Leu Pro Thr Lys Val
 325 330 335
 Pro Val Tyr Phe Thr Gly Lys Asp Gly Tyr Glu Thr Lys Asp Leu Thr
 340 345 350
 Val Glu Trp Glu Glu Val Pro Ala Glu Asn Leu Thr Lys Ala Gly Gln
 355 360 365
 Phe Thr Val Arg Gly Arg Val Leu Gly Ser Asn Leu Val Ala Glu Ile
 370 375 380
 Thr Val Arg Val Thr Asp Lys Leu Gly Glu Thr Leu Ser Asp Asn Pro
 385 390 395 400
 Asn Tyr Asp Glu Asn Ser Asn Gln Ala Phe Ala Ser Ala Thr Asn Asp
 405 410 415
 Ile Asp Lys Asn Ser His Asp Arg Val Asp Tyr Leu Asn Asp Gly Asp
 420 425 430
 His Ser Glu Asn Arg Arg Trp Thr Asn Trp Ser Pro Thr Pro Ser Ser
 435 440 445
 Asn Pro Glu Val Ser Ala Gly Val Ile Phe Arg Glu Asn Gly Lys Ile
 450 455 460
 Val Glu Arg Thr Val Thr Gln Gly Lys Val Gln Phe Phe Ala Asp Ser
 465 470 475 480
 Gly Thr Asp Ala Pro Ser Lys Leu Val Leu Glu Arg Tyr Val Gly Pro
 485 490 495
 Glu Phe Glu Val Pro Thr Tyr Tyr Ser Asn Tyr Gln Ala Tyr Asp Ala
 500 505 510
 Asp His Pro Phe Asn Asn Pro Glu Asn Trp Glu Ala Val Pro Tyr Arg
 515 520 525
 Ala Asp Lys Asp Ile Ala Ala Gly Asp Glu Ile Asn Val Thr Phe Lys
 530 535 540
 Ala Ile Lys Ala Lys Ala Met Arg Trp Arg Met Glu Arg Lys Ala Asp
 545 550 555 560
 Lys Ser Gly Val Ala Met Ile Glu Met Thr Phe Leu Ala Pro Ser Glu
 565 570 575

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Leu Pro Gln Glu Ser Thr Gln Ser Lys Ile Leu Val Asp Gly Lys Glu
 580 585 590
 Leu Ala Asp Phe Ala Glu Asn Arg Gln Asp Tyr Gln Ile Thr Tyr Lys
 595 600 605
 Gly Gln Arg Pro Lys Val Ser Val Glu Glu Asn Asn Gln Val Ala Ser
 610 615 620
 Thr Val Val Asp Ser Gly Glu Asp Ser Phe Pro Val Leu Val Arg Leu
 625 630 635 640
 Val Ser Glu Ser Gly Lys Gln Val Lys Glu Tyr Arg Ile His Leu Thr
 645 650 655
 Lys Glu Lys Pro Val Ser Glu Lys Thr Val Ala Ala Val Gln Glu Asp
 660 665 670
 Leu Pro Lys Ile Glu Phe Val Glu Lys Asp Leu Ala Tyr Lys Thr Val
 675 680 685
 Glu Lys Lys Asp Ser Thr Leu Tyr Leu Gly Glu Thr Arg Val Glu Gln
 690 695 700
 Glu Gly Lys Val Gly Lys Glu Arg Ile Phe Thr Ala Ile Asn Pro Asp
 705 710 715 720
 Gly Ser Lys Glu Glu Lys Leu Arg Glu Val Val Glu Val Pro Thr Asp
 725 730 735
 Arg Ile Val Leu Val Gly Thr Lys Pro Val Ala Gln Glu Ala Lys Lys
 740 745 750
 Pro Gln Val Ser Glu Lys Ala Asp Thr Lys Pro Ile Asp Ser Ser Glu
 755 760 765
 Ala Ser Gln Thr Asn Lys Ala Gln
 770 775

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

CTATCACTAT GTAAATAAAG AGATTATTC ACAAGAAGCT AAAGATTAA TTCAGACAGG 60
 AAAGCCTGAC AGGAATGAAG TTGTATATGG TTTGGTGTAT CAAAAGATC AGTTGCCTCA 120
 AACAGGGACA GAA 133

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Tyr His Tyr Val Asn Lys Glu Ile Ile Ser Gln Glu Ala Lys Asp Leu
1 5 10 15
Ile Gln Thr Gly Lys Pro Asp Arg Asn Glu Val Val Tyr Gly Leu Val
20 25 30
Tyr Gln Lys Asp Gln Leu Pro Gln Thr Gly Thr Glu
35 40

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 775 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

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TGAGACTCCT CAATCAATAA CAAATCAGGA GCAAGCTAGG ACAGAAAACC AAGTAGTAGA	60
GACAGAGGAA GCTCCAAAAG AAGAAGCACC TAAAACAGAA GAAAGTCCAA AGGAAGAACC	120
AAAATCGGAG GTAAAACCTA CTGACGACAC CCTTCCTAAA GTAGAAGAGG GGAAAGAAGA	180
TTCAGCAGAA CCAGCTCCAG TTGAAGAAGT AGGTGGAGAA GTTGAGTCAA AACCAAGAGG	240
AAAAGTAGCA GTTAAGCCAG AAAGTCAACC ATCAGACAAA CCAGCTGAGG AATCAAAAGT	300
TGAACAAGCA GGTGAACCAG TCGCGCCAAG AGAAGACGAA AAGGCACCAG TCGAGCCAGA	360
AAAGCAACCA GAAGCTCCTG AAGAAGAGAA GGCTGTAGAG GAAACACCGA AACAAGAAGA	420
GTCAACTCCA GATACCAAGG CTGAAGAAAC TGTAAGACCA AAAGAGGAGA CTGTTAATCA	480
ATCTATTGAA CAACCAAAAG TTGAAACGCC TGCTGTAGAA AAACAAACAG AACCAACAGA	540
GGAACCAAAA GTTGAACAAG CAGGTGAACC AGTCGCGCCA AGAGAAGACG AACAGGCACC	600
AACGGCACCA GTTGAGCCAG AAAAGCAACC AGAAGTTCCT GAAGAAGAGA AGGCTGTAGA	660
GGAAACACCG AAACCAGAAG ATAAAATAAA GGGTATTGGT ACTAAAGAAC CAGTTGATAA	720
AAGTGAGTTA AATAATCAAA TTGATAAAGC TAGTTCAGTT TCTCCTACTG ATTAT	775

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Glu Thr Pro Gln Ser Ile Thr Asn Gln Glu Gln Ala Arg Thr Glu Asn
 1 5 10 15
 Gln Val Val Glu Thr Glu Glu Ala Pro Lys Glu Glu Ala Pro Lys Thr
 20 25 30
 Glu Glu Ser Pro Lys Glu Glu Pro Lys Ser Glu Val Lys Pro Thr Asp
 35 40 45
 Asp Thr Leu Pro Lys Val Glu Gly Lys Glu Asp Ser Ala Glu Pro
 50 55 60
 Ala Pro Val Glu Glu Val Gly Gly Glu Val Glu Ser Lys Pro Glu Glu
 65 70 75 80
 Lys Val Ala Val Lys Pro Glu Ser Gln Pro Ser Asp Lys Pro Ala Glu
 85 90 95
 Glu Ser Lys Val Glu Gln Ala Gly Glu Pro Val Ala Pro Arg Glu Asp
 100 105 110
 Glu Lys Ala Pro Val Glu Pro Glu Lys Gln Pro Glu Ala Pro Glu Glu
 115 120 125
 Glu Lys Ala Val Glu Glu Thr Pro Lys Gln Glu Glu Ser Thr Pro Asp
 130 135 140
 Thr Lys Ala Glu Glu Thr Val Glu Pro Lys Glu Glu Thr Val Asn Gln
 145 150 155 160
 Ser Ile Glu Gln Pro Lys Val Glu Thr Pro Ala Val Glu Lys Gln Thr
 165 170 175
 Glu Pro Thr Glu Glu Pro Lys Val Glu Gln Ala Gly Glu Pro Val Ala
 180 185 190
 Pro Arg Glu Asp Glu Gln Ala Pro Thr Ala Pro Val Glu Pro Glu Lys
 195 200 205
 Gln Pro Glu Val Pro Glu Glu Glu Lys Ala Val Glu Glu Thr Pro Lys
 210 215 220
 Pro Glu Asp Lys Ile Lys Gly Ile Gly Thr Lys Glu Pro Val Asp Lys
 225 230 235 240
 Ser Glu Leu Asn Asn Gln Ile Asp Lys Ala Ser Ser Val Ser Pro Thr
 245 250 255
 Asp Tyr

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

241

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```

GGATGCTCAA GAAACTGCGG GAGTTCAC TA AATATGTG GCAGATTCAG AGCTATCATC      60
AGAAGAAAAG AAGCAGCTTG TCTATGATAT TCCGACATAC GTGGAGAATG ATGATGAAAC      120
TTATTATCTT GTTTATAAGT TAAATTCTCA AAATCAACTG GCGGAATTGC CAAATACTGG      180
AAGCAAGAAT GAGAGGCAA                                           199

```

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

a1
cont.

```

Asp Ala Gln Glu Thr Ala Gly Val His Tyr Lys Tyr Val Ala Asp Ser
1           5           10           15

Glu Leu Ser Ser Glu Glu Lys Lys Gln Leu Val Tyr Asp Ile Pro Thr
20           25           30

Tyr Val Glu Asn Asp Asp Glu Thr Tyr Tyr Leu Val Tyr Lys Leu Asn
35           40           45

Ser Gln Asn Gln Leu Ala Glu Leu Pro Asn Thr Gly Ser Lys Asn Glu
50           55           60

Arg Gln
65

```

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 835 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

CGACAAAGGT GAGACTGAGG TTCAACCAGA GTCGCCAGAT ACTGTGGTAA GTGATAAAGG      60
TGAACCAGAG CAGGTAGCAC CGCTTCCAGA ATATAAGGGT AATATTGAGC AAGTAAAACC      120

```

TGAAACTCCG GTTGAGAAGA CCAAAGAACA AGGTCCAGAA AAAACTGAAG AAGTTCCAGT 180
 AAAACCAACA GAAGAAACAC CAGTAAATCC AAATGAAGGT ACTACAGAAG GAACCTCAAT 240
 TCAAGAAGCA GAAAATCCAG TTCAACCTGC AGAAGAATCA ACAACGAATT CAGAGAAAGT 300
 ATCACCAGAT ACATCTAGCA AAAATACTGG GGAAGTGTCC AGTAATCCTA GTGATTTCGAC 360
 AACCTCAGTT GGAGAATCAA ATAAACCAGA ACATAATGAC TCTAAAAATG AAAATTTCAGA 420
 AAAAAGTGTG GAAGAAGTTC CAGTAAATCC AAATGAAGGC ACAGTAGAAG GTACCTCAAA 480
 TCAAGAAACA GAAAAACCAG TTCAACCTGC AGAAGAAACA CAAACAAACT CTGGGAAAAT 540
 AGCTAACGAA AATACTGGAG AAGTATCCAA TAAACCTAGT GATTCAAAAC CACCAGTTGA 600
 AGAATCAAAT CAACCAGAAA AAAACGGAAC TGCAACAAAA CCAGAAAATT CAGGTAATAC 660
 AACATCAGAG AATGGACAAA CAGAACCAGA ACCATCAAAC GGAAATTCAA CTGAGGATGT 720
 TTCAACCGAA TCAAACACAT CCAATTCAAA TGGAAACGAA GAAATTAAAC AAGAAAATGA 780
 ACTAGACCCT GATAAAAAGG TAGAAGAACC AGAGAAAACA CTTGAATTAA GAAAT 835

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 278 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp Lys Gly Glu Thr Glu Val Gln Pro Glu Ser Pro Asp Thr Val Val
 1 5 10 15
 Ser Asp Lys Gly Glu Pro Glu Gln Val Ala Pro Leu Pro Glu Tyr Lys
 20 25 30
 Gly Asn Ile Glu Gln Val Lys Pro Glu Thr Pro Val Glu Lys Thr Lys
 35 40 45
 Glu Gln Gly Pro Glu Lys Thr Glu Glu Val Pro Val Lys Pro Thr Glu
 50 55 60
 Glu Thr Pro Val Asn Pro Asn Glu Gly Thr Thr Glu Gly Thr Ser Ile
 65 70 75 80
 Gln Glu Ala Glu Asn Pro Val Gln Pro Ala Glu Glu Ser Thr Thr Asn
 85 90 95
 Ser Glu Lys Val Ser Pro Asp Thr Ser Ser Lys Asn Thr Gly Glu Val
 100 105 110
 Ser Ser Asn Pro Ser Asp Ser Thr Thr Ser Val Gly Glu Ser Asn Lys
 115 120 125

Pro Glu His Asn Asp Ser Lys Asn Glu Asn Ser Glu Lys Thr Val Glu
130 135 140

Glu Val Pro Val Asn Pro Asn Glu Gly Thr Val Glu Gly Thr Ser Asn
145 150 155 160

Gln Glu Thr Glu Lys Pro Val Gln Pro Ala Glu Glu Thr Gln Thr Asn
165 170 175

Ser Gly Lys Ile Ala Asn Glu Asn Thr Gly Glu Val Ser Asn Lys Pro
180 185 190

Ser Asp Ser Lys Pro Pro Val Glu Glu Ser Asn Gln Pro Glu Lys Asn
195 200 205

Gly Thr Ala Thr Lys Pro Glu Asn Ser Gly Asn Thr Thr Ser Glu Asn
210 215 220

Gly Gln Thr Glu Pro Glu Pro Ser Asn Gly Asn Ser Thr Glu Asp Val
225 230 235 240

Ser Thr Glu Ser Asn Thr Ser Asn Ser Asn Gly Asn Glu Glu Ile Lys
245 250 255

Gln Glu Asn Glu Leu Asp Pro Asp Lys Lys Val Glu Glu Pro Glu Lys
260 265 270

Thr Leu Glu Leu Arg Asn
275

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 709 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAATCAATTG GTAGCACAAG ATCCAAAAGC ACAAGATAGC ACTAAACTGA CTGCTGAAAA 60

ATCAACTGTT AAAGCACCTG CTCAAAGAGT AGATGTAAAA GATATAACTC ATTTAACAGA 120

TGAAGAAAAA GTTAAGGTTG CTATTTTACA AGCAAATGGT TCAGCATTAG ACGGAGCGAC 180

AATCAATGTA GCTGGAGATG GTACAGCAAC AATCACATTC CCAGATGGTT CAGTAGTGAC 240

GATTCTAGGA AAAGATACAG TTCAACAATC TGCGAAAGGT GAATCTGTAA CTCAAGAAGC 300

TACACCAGAG TATAAGCTAG AAAATACACC AGGTGGAGAT AAGGGAGGCA ATACTGGAAG 360

CTCAGATGCT AATGCGAATG AAGGCGGTGG TAGCCAGGCG GGTGGATCAG CTCACACAGG 420

TTCAACAAAAC TCAGCTCAAT CACAAGCTTC TAAGCAATTA GCTACTGAAA AAGAATCAGC 480

TAAAAATGCC ATTGAAAAAG CAGCCAAGGA CAAGCAGGAT GAAATCAAAG GCGCACCCT 540

TTCTGATAAA GAAAAAGCAG AACTTTTAGC AAGAGTGGAA GCAGAAAAAC AAGCAGCTCT 600

CAAAGAGATT GAAATGCGA AACTATGGA AGATGTGAAG GAAGCAGAAA CGATTGGAGT 660

GCAAGCCATT GCCATGGTTA CAGTTCCTAA GAGACCAGTG GCTCCTAAT

709

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Asn Gln Leu Val Ala Gln Asp Pro Lys Ala Gln Asp Ser Thr Lys Leu
 1 5 10 15
 Thr Ala Glu Lys Ser Thr Val Lys Ala Pro Ala Gln Arg Val Asp Val
 20 25 30
 Lys Asp Ile Thr His Leu Thr Asp Glu Glu Lys Val Lys Val Ala Ile
 35 40 45
 Leu Gln Ala Asn Gly Ser Ala Leu Asp Gly Ala Thr Ile Asn Val Ala
 50 55 60
 Gly Asp Gly Thr Ala Thr Ile Thr Phe Pro Asp Gly Ser Val Val Thr
 65 70 75 80
 Ile Leu Gly Lys Asp Thr Val Gln Gln Ser Ala Lys Gly Glu Ser Val
 85 90 95
 Thr Gln Glu Ala Thr Pro Glu Tyr Lys Leu Glu Asn Thr Pro Gly Gly
 100 105 110
 Asp Lys Gly Gly Asn Thr Gly Ser Ser Asp Ala Asn Ala Asn Glu Gly
 115 120 125
 Gly Gly Ser Gln Ala Gly Gly Ser Ala His Thr Gly Ser Gln Asn Ser
 130 135 140
 Ala Gln Ser Gln Ala Ser Lys Gln Leu Ala Thr Glu Lys Glu Ser Ala
 145 150 155 160
 Lys Asn Ala Ile Glu Lys Ala Ala Lys Asp Lys Gln Asp Glu Ile Lys
 165 170 175
 Gly Ala Pro Leu Ser Asp Lys Glu Lys Ala Glu Leu Leu Ala Arg Val
 180 185 190
 Glu Ala Glu Lys Gln Ala Ala Leu Lys Glu Ile Glu Asn Ala Lys Thr
 195 200 205
 Met Glu Asp Val Lys Glu Ala Glu Thr Ile Gly Val Gln Ala Ile Ala
 210 215 220
 Met Val Thr Val Pro Lys Arg Pro Val Ala Pro Asn
 225 230 235

215

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CAAACAGTCA GCTTCAGGAA CGATTGAGGT GATTTCACGA GAAAATGGCT CTGGGACACG 60
GGGTGCCTTC ACAGAAATCA CAGGGATTCT CAAAAAAGAC GGTGATAAAA AAATTGACAA 120
CACTGCCAAA ACAGCTGTGA TTCAAATAG TACAGAAGGT GTTCTCTCAG CAGTTCAAGG 180
GAATGCTAAT GCTATCGGCT ACATCTCCTT GGGATCTTTA ACGAAATCTG TCAAGGCTTT 240
AGAGATTGAT GGTGTCAAGG CTAGTCGAGA CACAGTTTTA GATGGTGAAT ACCCTCTTCA 300
ACGTCCCTTC AACATTGTTT GGTCTTCTAA TCTTTCCAAG CTAGGTCAAG ATTTTATCAG 360
CTTTATCCAC TCCAAACAAG GTCAACAAGT GGTACAGAT AATAAATTTA TTGAAGCTAA 420
AACCGAAACC ACGGAATATA CAAGCCAACA CTTATCAGGC AAGTTGTCTG TTGTAGGTTC 480
CACTTCAGTA TCTTCTTTAA TGGAAAAATT AGCAGAAGCT TATAAAAAAG AAAATCCAGA 540
AGTTACGATT GATATTACCT CTAATGGGTC TTCAGCAGGT ATTACCGCTG TTAAGGAGAA 600
AACCGCTGAT ATTGGTATGG TTTCTAGGGA ATTAACCTCT GAAGAAGGTA AGAGTCTCAC 660
CCATGATGCT ATTGCTTTAG ACGGTATTGC TGTGTGGTC AATAATGACA ATAAGGCAAG 720
CCAAGTCAGT ATGGCTGAAC TTGCAGACGT TTTTAGTGGC AAATTAACCA CCTGGGACAA 780
GATTAAA 787

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Lys Gln Ser Ala Ser Gly Thr Ile Glu Val Ile Ser Arg Glu Asn Gly
1 5 10 15
Ser Gly Thr Arg Gly Ala Phe Thr Glu Ile Thr Gly Ile Leu Lys Lys
20 25 30
Asp Gly Asp Lys Lys Ile Asp Asn Thr Ala Lys Thr Ala Val Ile Gln
35 40 45

Asn Ser Thr Glu Gly Val Leu Ser Ala Val Gln Gly Asn Ala Asn Ala
 50 55 60
 Ile Gly Tyr Ile Ser Leu Gly Ser Leu Thr Lys Ser Val Lys Ala Leu
 65 70 75 80
 Glu Ile Asp Gly Val Lys Ala Ser Arg Asp Thr Val Leu Asp Gly Glu
 85 90 95
 Tyr Pro Leu Gln Arg Pro Phe Asn Ile Val Trp Ser Ser Asn Leu Ser
 100 105 110
 Lys Leu Gly Gln Asp Phe Ile Ser Phe Ile His Ser Lys Gln Gly Gln
 115 120 125
 Gln Val Val Thr Asp Asn Lys Phe Ile Glu Ala Lys Thr Glu Thr Thr
 130 135 140
 Glu Tyr Thr Ser Gln His Leu Ser Gly Lys Leu Ser Val Val Gly Ser
 145 150 155 160
 Thr Ser Val Ser Ser Leu Met Glu Lys Leu Ala Glu Ala Tyr Lys Lys
 165 170 175
 Glu Asn Pro Glu Val Thr Ile Asp Ile Thr Ser Asn Gly Ser Ser Ala
 180 185 190
 Gly Ile Thr Ala Val Lys Glu Lys Thr Ala Asp Ile Gly Met Val Ser
 195 200 205
 Arg Glu Leu Thr Pro Glu Glu Gly Lys Ser Leu Thr His Asp Ala Ile
 210 215 220
 Ala Leu Asp Gly Ile Ala Val Val Val Asn Asn Asp Asn Lys Ala Ser
 225 230 235 240
 Gln Val Ser Met Ala Glu Leu Ala Asp Val Phe Ser Gly Lys Leu Thr
 245 250 255
 Thr Trp Asp Lys Ile Lys
 260

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

ATTCGATGAT GCGGATGAAA AGATGACCCG TGATGAAATT GCCTATATGC TGACAAATAG 60
 TGAAGAAACA TTGGATGCTG ATGAGATTGA GATGCTACAA GGTGCTTTT CGCTCGATGA 120
 ACTGATGGCA CGAGAGGTTA TGGTTCTCG AACGGATGCC TTTATGGTGG ATATTCAGGA 180
 TGATAGTCAA GCCATTATCC AAAGTATTTT AAAACAAAAT TATTCTCGTA TCCCGGTTTA 240

TGATGGGGAT AAGGACAATG TAATTGGAAT CATTACACACC AAGAGTCTCC TTAAGGCAGG 300
 CTTTGTGGAC GGTTTTGACA ATATTGTTTG GAAGAGAATT TTACAAGATC CACTTTTGTG 360
 ACCTGAAACT ATTTTGTGG ATGACTTGCT AAAAGAACTG CGAAATACCC AAAGACAAAT 420
 G 421

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Phe Asp Asp Ala Asp Glu Lys Met Thr Arg Asp Glu Ile Ala Tyr Met
 1 5 10 15
 Leu Thr Asn Ser Glu Glu Thr Leu Asp Ala Asp Glu Ile Glu Met Leu
 20 25 30
 Gln Gly Val Phe Ser Leu Asp Glu Leu Met Ala Arg Glu Val Met Val
 35 40 45
 Pro Arg Thr Asp Ala Phe Met Val Asp Ile Gln Asp Asp Ser Gln Ala
 50 55 60
 Ile Ile Gln Ser Ile Leu Lys Gln Asn Tyr Ser Arg Ile Pro Val Tyr
 65 70 75 80
 Asp Gly Asp Lys Asp Asn Val Ile Gly Ile Ile His Thr Lys Ser Leu
 85 90 95
 Leu Lys Ala Gly Phe Val Asp Gly Phe Asp Asn Ile Val Trp Lys Arg
 100 105 110
 Ile Leu Gln Asp Pro Leu Phe Val Pro Glu Thr Ile Phe Val Asp Asp
 115 120 125
 Leu Leu Lys Glu Leu Arg Asn Thr Gln Arg Gln Met
 130 135 140

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

GGAGAGTCGA TCAAAAGTAG ATGAAGCTGT GTCTAAGTTT GAAAAGGACT CATCTTCTTC 60

GTCAAGTTCA GACTCTTCCA CTAAACCGGA AGCTTCAGAT ACAGCGAAGC CAAACAAGCC 120
 GACAGAACCA GGAGAAAAGG TAGCAGAAGC TAAGAAGAAG GTTGAAGAAG CTGAGAAAAA 180
 AGCCAAGGAT CAAAAAGAAG AAGATCGTCG TAACTACCCA ACCATTACTT AAAAAACGCT 240
 TGAACCTGAA ATTGCTGAGT CCGATGTGGA AGTTAAAAAA GCGGAGCTTG AACTAGTAAA 300
 AGTGAAAGCT AACGAACCTC GAGACGAGCA A 331

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Glu Ser Arg Ser Lys Val Asp Glu Ala Val Ser Lys Phe Glu Lys Asp
 1 5 10 15
 Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Thr Lys Pro Glu Ala Ser
 20 25 30
 Asp Thr Ala Lys Pro Asn Lys Pro Thr Glu Pro Gly Glu Lys Val Ala
 35 40 45
 Glu Ala Lys Lys Lys Val Glu Glu Ala Glu Lys Lys Ala Lys Asp Gln
 50 55 60
 Lys Glu Glu Asp Arg Arg Asn Tyr Pro Thr Ile Thr Tyr Lys Thr Leu
 65 70 75 80
 Glu Leu Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala Glu Leu
 85 90 95
 Glu Leu Val Lys Val Lys Ala Asn Glu Pro Arg Asp Glu Gln
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

ATGGACAACA GGAAACTGGG ACGAGGTTAT ATCTGGTAAG ATTGACAAAGT ACAAAGATCC 60
 AGATATTCCA ACAGTTGAAT CACAAGAAGT TACGTCAGAC TCTAGTGATA AAGAAATAAC 120

GGTAAGGTAT GACCGTTTAT CAACACCAGA AAAACCAATC CCACAACCAA ATCCAGAGCA 180
 TCCAAGTGTT CCGACACCAA ACCCAGAACT ACCAAATCAA GAGACTCCAA CACCAGATAA 240
 ACCAACTCCA GAACCAGGTA CTCCAAAAAC TGAAACTCCA GTGAATCCAG ACCCAGAAGT 300
 TCCGACTTAT GAGACAGGTA AGAGAGAGGA ATTGCCAAAC ACAGGTACAG AAGCTAAT 358

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Trp Thr Thr Gly Asn Trp Asp Glu Val Ile Ser Gly Lys Ile Asp Lys
 1 5 10 15
 Tyr Lys Asp Pro Asp Ile Pro Thr Val Glu Ser Gln Glu Val Thr Ser
 20 25 30
 Asp Ser Ser Asp Lys Glu Ile Thr Val Arg Tyr Asp Arg Leu Ser Thr
 35 40 45
 Pro Glu Lys Pro Ile Pro Gln Pro Asn Pro Glu His Pro Ser Val Pro
 50 55 60
 Thr Pro Asn Pro Glu Leu Pro Asn Gln Glu Thr Pro Thr Pro Asp Lys
 65 70 75 80
 Pro Thr Pro Glu Pro Gly Thr Pro Lys Thr Glu Thr Pro Val Asn Pro
 85 90 95
 Asp Pro Glu Val Pro Thr Tyr Glu Thr Gly Lys Arg Glu Glu Leu Pro
 100 105 110
 Asn Thr Gly Thr Glu Ala Asn
 115

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CGATGGGCTC AATCCAACCC CAGGTCAAGT CTTACCTGAA GAGACATCGG GAACGAAAGA 60
 GGGTGACTTA TCAGAAAAAC CAGGAGACAC CGTTCTCACT CAAGCGAAAC CTGAGGGCGT 120

TACTGGAAAT ACGAATTCAC TTCCGACACC TACAGAAAGA ACTGAAGTGA GCGAGGAAAC 180
 AAGCCCTTCT AGTCTGGATA CACTTTTGA AAAAGATGAA GAAGCTCAA AAAATCCAGA 240
 GCTAACAGAT GTCTTAAAAG AAAGTGTAGA TACAGCTGAT GTGGATGGGA CACAAGCAAG 300
 TCCAGCAGAA ACTACTCCTG AACAAGTAAA AGGTGGAGTG AAAGAAAATA CAAAAGACAG 360
 CATCGATGTT CCTGCTGCTT ATCTTGAAAA AGCTGAAGGG AAAGGTCCTT TCACTGCCGG 420
 TGTAAACCAA GTAATTCCTT ATGAACATTT CGCTGGTGAT GGTATGTTAA CTCGTCTATT 480
 ACTAAAAGCT TCGGATAATG CTCCTTGGTC TGACAATGGT ACTGCTAAAA ATCCTGCTTT 540
 ACCTCCTCTT GAAGGATTAA CAAAAGGGAA ATACTTCTAT GAAGTAGACT TAAATGGCAA 600
 TACTGTTGGT AAACAAGGTC AAGCTTTAAT TGATCAACTT CGCGCTAATG GTACTCAAAC 660
 TTATAAAGCT ACTGTTAAAG TTTACGAAA TAAAGACGGT AAAGCTGACT TGAATAATCT 720
 AGTTGCTACT AAAAATGTAG ACATCAACAT CAATGGATTA GTTGCTAAAG AACAGTTCA 780
 AAAAGCCGTT GCAGACAACG TTAAAGACAG TATCGATGTT CCAGCAGCCT ACCTAGAAAA 840
 AGCCAAGGTT GAAGGTCCAT TCACAGCAGG TGTCAACCAT GTGATTCCAT ACGAACTCTT 900
 CGCAGGTGAT GGCATGTTGA CTCGTCTCTT GCTCAAGGCA TCTGACAAGG CACCATGGTC 960
 AGATAACGGC GACGCTAAAA ACCCAGCCCT ATCTCCACTA GGCGAAAACG TGAAGACCAA 1020
 AGGTCAATAC TTCTATCAAN TAGCCTTGGA CGGAAATGTA GCTGGCAAAG AAAACAAGC 1080
 GCTCATTGAC CAGTTCCGAG CAAANGGTAC TCAAACCTTAC AGCGCTACAG TCAATGTCTA 1140
 TGGTAACAAA GACGGTAAAC CAGACTTGGA CAACATCGTA GCAACTAAAA AAGTCACTAT 1200
 TAACATAAAC GGTTTAATTT CTAAAGAAAC AGTTCAAAAA GCCGTTGCAG ACAACGTTAA 1260
 NGACAGTATC GATGTTCCAG CAGCCTACCT AGAAAAAGCC AAGGGTGAAG GTCCATTAC 1320
 AGCAGGTGTC AACCATGTGA TTCCATACGA ACTCTTCGCA GGTGATGGTA TGTGACTCG 1380
 TCTCTTGCTC AAGGCATCTG ACAAGGCACC ATGGTCAGAT AACGNGACG CTAAAAACCC 1440
 AGCNCATCTT CCACTAGGTG AAAACGTGAA GACCAAAGGT CAATACTTCT ATCAANTAGC 1500
 CTTGGACGGA AATGTAGCTG GCAAAGAAAA ACAAGCGCTC ATTGACCAGT TCCGAGCAA 1560
 CGGTACTCAA ACTTACAGCG CTACAGTCAA TGTCTATGGT AACAAAGACG GTAAACCAGA 1620
 CTTGGACAAC ATCGTAGCAA CTAAAAAGT CACTATTAAG ATAAATGTTA AAGAAACATC 1680
 AGACACAGCA AATGGTTTCAT TATCACCTTC TAACTCTGGT TCTGGCGTGA CTCCGATGAA 1740
 TCACAATCAT GCTACAGGTA CTACAGATAG CATGCCTGCT GACACCATGA CAAGTTCTAC 1800
 CAACACGATG GCAGGTGAAA ACATGGCTGC TTCTGCTAAC AAGATGTCTG ATACGATGAT 1860
 GTCAGAGGAT AAAGCTATG 1879

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Asp Gly Leu Asn Pro Thr Pro Gly Gln Val Leu Pro Glu Glu Thr Ser
 1 5 10 15
 Gly Thr Lys Glu Gly Asp Leu Ser Glu Lys Pro Gly Asp Thr Val Leu
 20 25 30
 Thr Gln Ala Lys Pro Glu Gly Val Thr Gly Asn Thr Asn Ser Leu Pro
 35 40 45
 Thr Pro Thr Glu Arg Thr Glu Val Ser Glu Glu Thr Ser Pro Ser Ser
 50 55 60
 Leu Asp Thr Leu Phe Glu Lys Asp Glu Glu Ala Gln Lys Asn Pro Glu
 65 70 75 80
 Leu Thr Asp Val Leu Lys Glu Thr Val Asp Thr Ala Asp Val Asp Gly
 85 90 95
 Thr Gln Ala Ser Pro Ala Glu Thr Thr Pro Glu Gln Val Lys Gly Gly
 100 105 110
 Val Lys Glu Asn Thr Lys Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu
 115 120 125
 Glu Lys Ala Glu Gly Lys Gly Pro Phe Thr Ala Gly Val Asn Gln Val
 130 135 140
 Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu
 145 150 155 160
 Leu Lys Ala Ser Asp Asn Ala Pro Trp Ser Asp Asn Gly Thr Ala Lys
 165 170 175
 Asn Pro Ala Leu Pro Pro Leu Glu Gly Leu Thr Lys Gly Lys Tyr Phe
 180 185 190
 Tyr Glu Val Asp Leu Asn Gly Asn Thr Val Gly Lys Gln Gly Gln Ala
 195 200 205
 Leu Ile Asp Gln Leu Arg Ala Asn Gly Thr Gln Thr Tyr Lys Ala Thr
 210 215 220
 Val Lys Val Tyr Gly Asn Lys Asp Gly Lys Ala Asp Leu Thr Asn Leu
 225 230 235 240
 Val Ala Thr Lys Asn Val Asp Ile Asn Ile Asn Gly Leu Val Ala Lys
 245 250 255
 Glu Thr Val Gln Lys Ala Val Ala Asp Asn Val Lys Asp Ser Ile Asp
 260 265 270

Val Pro Ala Ala Tyr Leu Glu Lys Ala Lys Gly Glu Gly Pro Phe Thr
 275 280 285
 Ala Gly Val Asn His Val Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly
 290 295 300
 Met Leu Thr Arg Leu Leu Leu Lys Ala Ser Asp Lys Ala Pro Trp Ser
 305 310 315 320
 Asp Asn Gly Asp Ala Lys Asn Pro Ala Leu Ser Pro Leu Gly Glu Asn
 325 330 335
 Val Lys Thr Lys Gly Gln Tyr Phe Tyr Gln Xaa Ala Leu Asp Gly Asn
 340 345 350
 Val Ala Gly Lys Glu Lys Gln Ala Leu Ile Asp Gln Phe Arg Ala Xaa
 355 360 365
 Gly Thr Gln Thr Tyr Ser Ala Thr Val Asn Val Tyr Gly Asn Lys Asp
 370 375 380
 Gly Lys Pro Asp Leu Asp Asn Ile Val Ala Thr Lys Lys Val Thr Ile
 385 390 395 400
 Asn Ile Asn Gly Leu Ile Ser Lys Glu Thr Val Gln Lys Ala Val Ala
 405 410 415
 Asp Asn Val Xaa Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu Glu Lys
 420 425 430
 Ala Lys Gly Glu Gly Pro Phe Thr Ala Gly Val Asn His Val Ile Pro
 435 440 445
 Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu Leu Lys
 450 455 460
 Ala Ser Asp Lys Ala Pro Trp Ser Asp Asn Gly Asp Ala Lys Asn Pro
 465 470 475 480
 Ala Leu Ser Pro Leu Gly Glu Asn Val Lys Thr Lys Gly Gln Tyr Phe
 485 490 495
 Tyr Gln Xaa Ala Leu Asp Gly Asn Val Ala Gly Lys Glu Lys Gln Ala
 500 505 510
 Leu Ile Asp Gln Phe Arg Ala Asn Gly Thr Gln Thr Tyr Ser Ala Thr
 515 520 525
 Val Asn Val Tyr Gly Asn Lys Asp Gly Lys Pro Asp Leu Asp Asn Ile
 530 535 540
 Val Ala Thr Lys Lys Val Thr Ile Lys Ile Asn Val Lys Glu Thr Ser
 545 550 555 560
 Asp Thr Ala Asn Gly Ser Leu Ser Pro Ser Asn Ser Gly Ser Gly Val
 565 570 575
 Thr Pro Met Asn His Asn His Ala Thr Gly Thr Thr Asp Ser Met Pro
 580 585 590
 Ala Asp Thr Met Thr Ser Ser Thr Asn Thr Met Ala Gly Glu Asn Met
 595 600 605

Ala Ala Ser Ala Asn Lys Met Ser Asp Thr Met Met Ser Glu Asp Lys
 610 615 620

Ala Met
 625

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 593 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

TTCCAATCAA AAACAGGCAG ATGGTAAACT CAATATCGTG ACAACCTTTT ACCCTGTCTA 60
 TGAATTTACC AAGCAAGTCG CAGGAGATAC GGCTAATGTA GAACTCCTAA TCGGTGCTGG 120
 GACAGAACCT CATGAATACG AACCATCTGC CAAGGCAGTT GCCAAAATCC AAGATGCAGA 180
 TACCTTCGTT TATGAAAATG AAAACATGGA AACATGGGTA CCTAAATTGC TAGATACCTT 240
 GGATAAGAAA AAAGTGAAAA CCATCAAGGC GACAGGCGAT ATGTTGCTCT TGCCAGGTGG 300
 CGAGGAAGAA GAGGGAGACC ATGACCATGG AGAAGAAGGT CATCACCATG AGTTTGACCC 360
 CCATGTTTGG TTATCACCAG TTCGTGCCAT TAAACTAGTA GAGCACCATC CGCGACACTT 420
 GTCAGCAGAT TATCCTGATA AAAAAGAGAC CTTTGAGAAG AATGCAGCTG CCTATATCGA 480
 AAAATTGCAA GCCTTGATA AGGCTTACGC AGAAGGTTTG TCTCAAGCAA AACAAAAGAG 540
 CTTTGTGACT CAACACGCAG CTTTAACTa TCTTGCCTTG GACTATGGGA CTC 593

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 197 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Ser Asn Gln Lys Gln Ala Asp Gly Lys Leu Asn Ile Val Thr Thr Phe
 1 5 10 15
 Tyr Pro Val Tyr Glu Phe Thr Lys Gln Val Ala Gly Asp Thr Ala Asn
 20 25 30
 Val Glu Leu Leu Ile Gly Ala Gly Thr Glu Pro His Glu Tyr Glu Pro
 35 40 45
 Ser Ala Lys Ala Val Ala Lys Ile Gln Asp Ala Asp Thr Phe Val Tyr

50		55		60
Glu Asn Glu Asn Met Glu Thr Trp Val Pro Lys Leu Leu Asp Thr Leu				
65		70		75 80
Asp Lys Lys Lys Val Lys Thr Ile Lys Ala Thr Gly Asp Met Leu Leu				
	85		90	95
Leu Pro Gly Gly Glu Glu Glu Glu Gly Asp His Asp His Gly Glu Glu				
	100		105	110
Gly His His His Glu Phe Asp Pro His Val Trp Leu Ser Pro Val Arg				
	115		120	125
Ala Ile Lys Leu Val Glu His His Pro Arg His Leu Ser Ala Asp Tyr				
	130		135	140
Pro Asp Lys Lys Glu Thr Phe Glu Lys Asn Ala Ala Ala Tyr Ile Glu				
	145		150	155 160
Lys Leu Gln Ala Leu Asp Lys Ala Tyr Ala Glu Gly Leu Ser Gln Ala				
	165		170	175
Lys Gln Lys Ser Phe Val Thr Gln His Ala Ala Phe Asn Tyr Leu Ala				
	180		185	190
Leu Asp Tyr Gly Thr				
	195			

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1003 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

TATCACAGGA TCGAACGGTA AGACAACCAC AACGACTATG ATTGGGGAAG TTTTGACTGC	60
TGCTGGCCAA CATGGTCTTT TATCAGGGAA TATCGGCTAT CCAGCTAGTC AGGTGCTCA	120
AATAGCATCA GATAAGGACA CGCTTGTAT GGAACCTTCT TCTTTCCAAC TCATGGGTGT	180
TCAAGAATTC CATCCAGAGA TTGCGGTAT TACCAACCTC ATGCCAACTC ATATCGACTA	240
CCATGGGTCA TTTTCGGAAT ATGTAGCAGC CAAGTGAAT ATCCAGAACA AGATGACAGC	300
AGCTGATTTT CTTGTCTTGA ACTTTAATCA AGACTTGGCA AAAGACTTGA CTTCCAAGAC	360
AGAAGCCACT GTTGATACCAT TTTCAACACT TGAAAAGGTT GATGGAGCTT ATCTGGAAGA	420
TGGTCAACTC TACTTCCGTG GTGAAGTAGT CATGGCAGCG AATGAAATCG GTGTCCAGG	480
TAGCCACAAT GTGGAAAATG CCCTTGCGAC TATTGCTGTA GCCAAGCTTC GTGATGTGGA	540
CAATCAAACC ATCAAGGAAA CTCTTTCAGC CTTGGGTGGT GTCAAACACC GTCTCCAGTT	600
TGTGGATGAC ATCAAGGGTG TTAAATTCTA TAACGACAGT AAATCAACTA ATATCTTGGC	660

TACTCAAAAA GCCTTGTCTAG GATTTGACAA CAGCAAGGTC GTCTTGATTG CAGGTGGTTT 720
 GGACCGTGGC AATGAGTTTG ACGAATTGGT GCCAGACATT ACTGGACTCA AGAAGATGGT 780
 CATCCTGGGT CAATCTGCAG AACGTGTCAA ACGGGCAGCA GACAAGGCTG GTGTCGCTTA 840
 TGTGGAGGCG ACAGATATTG CAGATGCGAC CCGCAAGGCC TATGAGCTTG CGACTCAAGG 900
 AGATGTGGTT CTTCTTAGTC CTGCCAATGC TAGCTGGGAT ATGTATGCTA ACTTTGAAGT 960
 ACGTGGCGAC CTCATTATCG ACACAGTAGC GGAGTTAAAA GAA 1003

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Gly Ile Thr Gly Ser Asn Gly Lys Thr Thr Thr Thr Thr Met Ile Gly
 1 5 10 15
 Glu Val Leu Thr Ala Ala Gly Gln His Gly Leu Leu Ser Gly Asn Ile
 20 25 30
 Gly Tyr Pro Ala Ser Gln Val Ala Gln Ile Ala Ser Asp Lys Asp Thr
 35 40 45
 Leu Val Met Glu Leu Ser Ser Phe Gln Leu Met Gly Val Gln Glu Phe
 50 55 60
 His Pro Glu Ile Ala Val Ile Thr Asn Leu Met Pro Thr His Ile Asp
 65 70 75 80
 Tyr His Gly Ser Phe Ser Glu Tyr Val Ala Ala Lys Trp Asn Ile Gln
 85 90 95
 Asn Lys Met Thr Ala Ala Asp Phe Leu Val Leu Asn Phe Asn Gln Asp
 100 105 110
 Leu Ala Lys Asp Leu Thr Ser Lys Thr Glu Ala Thr Val Val Pro Phe
 115 120 125
 Ser Thr Leu Glu Lys Val Asp Gly Ala Tyr Leu Glu Asp Gly Gln Leu
 130 135 140
 Tyr Phe Arg Gly Glu Val Val Met Ala Ala Asn Glu Ile Gly Val Pro
 145 150 155 160
 Gly Ser His Asn Val Glu Asn Ala Leu Ala Thr Ile Ala Val Ala Lys
 165 170 175
 Leu Arg Asp Val Asp Asn Gln Thr Ile Lys Glu Thr Leu Ser Ala Phe
 180 185 190

Gly Gly Val Lys His Arg Leu Gln Phe Val Asp Asp Ile Lys Gly Val
 195 200 205

Lys Phe Tyr Asn Asp Ser Lys Ser Thr Asn Ile Leu Ala Thr Gln Lys
 210 215 220

Ala Leu Ser Gly Phe Asp Asn Ser Lys Val Val Leu Ile Ala Gly Gly
 225 230 235 240

Leu Asp Arg Gly Asn Glu Phe Asp Glu Leu Val Pro Asp Ile Thr Gly
 245 250 255

Leu Lys Lys Met Val Ile Leu Gly Gln Ser Ala Glu Arg Val Lys Arg
 260 265 270

Ala Ala Asp Lys Ala Gly Val Ala Tyr Val Glu Ala Thr Asp Ile Ala
 275 280 285

Asp Ala Thr Arg Lys Ala Tyr Glu Leu Ala Thr Gln Gly Asp Val Val
 290 295 300

Leu Leu Ser Pro Ala Asn Ala Ser Trp Asp Met Tyr Ala Asn Phe Glu
 305 310 315 320

Val Arg Gly Asp Leu Phe Ile Asp Thr Val Ala Glu Leu Lys Glu
 325 330 335

(2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

AAGTTCATCG AAGATGGTTG GGAAGTCCAC TATATCGGGG ACAAGTGTGG TATCGAACAC 60

CAAGAAATCC TTAAGTCAGG TTTGGATGTC ACCTTCCATT CTATTGCGAC TGGAAAATTG 120

CGTCGCTATT TCTCTGGCA AAATATGCTG GACGTCTTCA AAGTTGGTTG GGAATTGTC 180

CAATCGCTCT TTATCATGTT GCGACTGCGT CCACAGACCC TTTTTCAAA GGGGGGCTTT 240

GTCTCAGTAC CGCTGTTAT CGCTGCGGT GTGTCAGGAG TGCCTGTCTT TATTCACGAA 300

TCTGACCTGT CTATGGGCTT GGCCAATAAA ATCGCCTATA AATTTGCGAC TAAGATGTAT 360

TCAACCTTTG AACAAGCTTC GAGTTTGGCT AAGGTTGAGC ATGTGGGAGC GG 412

(2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Ser Ser Ser Lys Met Val Gly Lys Ser Thr Ile Ser Gly Thr Ser Val
 1 5 10 15

Val Ser Asn Thr Lys Lys Ser Leu Ser Gln Val Trp Met Ser Pro Ser
 20 25 30

Ile Leu Leu Arg Leu Glu Asn Cys Val Ala Ile Ser Leu Gly Lys Ile
 35 40 45

Cys Trp Thr Ser Ser Lys Leu Val Gly Glu Leu Ser Asn Arg Ser Leu
 50 55 60

Ser Cys Cys Asp Cys Val His Arg Pro Phe Phe Gln Arg Gly Ala Leu
 65 70 75 80

Ser Gln Tyr Arg Leu Leu Ser Leu Arg Val Cys Gln Glu Cys Leu Ser
 85 90 95

Leu Phe Thr Asn Leu Thr Cys Leu Trp Ala Trp Pro Ile Lys Ser Pro
 100 105 110

Ile Asn Leu Arg Leu Arg Cys Ile Gln Pro Leu Asn Lys Leu Arg Val
 115 120 125

Trp Leu Arg Leu Ser Met Trp Glu Arg
 130 135

(2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 544 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

ATCGCTAGCT AGTGAAATGC AAGAAAGTAC ACGTAAATTC AAGGTTACTG CTGACCTAAC 60

AGATGCCGGT GTTGAACGA TTGAAGTTCC TTTGAGCATT GAAGATTTAC CCAATGGGCT 120

GACCGCTGTG GCGACTCCGC AAAAAATTAC AGTCAAGATT GGTAAGAAGG CTCAGAAGGA 180

TAAGGTAAAG ATTGTACCAG AGATTGACCC TAGTCAAATT GATAGTCGGG TACAAATTGA 240

AAATGTCATG GTGTCAGATA AAGAAGTGTC TATTACGAGT GACCAAGAGA CATTGGATAG 300

AATTGATAAG ATTATCGCTG TTTTGCCAAC TAGCGAACGT ATAACAGGTA ATTACAGTGG 360

TTCAGTACCT TTGCAGGCAA TCGACCGCAA TGGTGTGTG TTTACCGCAG TTATCACTCC 420

GTTTGATACA ATAATGAAGG TGA CTACAAA ACCAGTAGCA CCAAGTTCAA GCACATCAAA 480

TTCAAGTACA AGCAGTTCAT CGGAGACATC TTCGTCAACG AAAGCAACTA GTTCAAAAAC 540

GAAT 544

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 181 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Ser Leu Ala Ser Glu Met Gln Glu Ser Thr Arg Lys Phe Lys Val Thr
 1 5 10 15
 Ala Asp Leu Thr Asp Ala Gly Val Gly Thr Ile Glu Val Pro Leu Ser
 20 25 30
 Ile Glu Asp Leu Pro Asn Gly Leu Thr Ala Val Ala Thr Pro Gln Lys
 35 40 45
 Ile Thr Val Lys Ile Gly Lys Lys Ala Gln Lys Asp Lys Val Lys Ile
 50 55 60
 Val Pro Glu Ile Asp Pro Ser Gln Ile Asp Ser Arg Val Gln Ile Glu
 65 70 75 80
 Asn Val Met Val Ser Asp Lys Glu Val Ser Ile Thr Ser Asp Gln Glu
 85 90 95
 Thr Leu Asp Arg Ile Asp Lys Ile Ile Ala Val Leu Pro Thr Ser Glu
 100 105 110
 Arg Ile Thr Gly Asn Tyr Ser Gly Ser Val Pro Leu Gln Ala Ile Asp
 115 120 125
 Arg Asn Gly Val Val Leu Pro Ala Val Ile Thr Pro Phe Asp Thr Ile
 130 135 140
 Met Lys Val Thr Thr Lys Pro Val Ala Pro Ser Ser Ser Thr Ser Asn
 145 150 155 160
 Ser Ser Thr Ser Ser Ser Ser Glu Thr Ser Ser Ser Thr Lys Ala Thr
 165 170 175
 Ser Ser Lys Thr Asn
 180

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GCACCAGATG GGGCACAAGG TTCAGGGATC AGATGTTGAA AAGTACTACT TTACCCAACG 60
 CGGTCTTGAG CAGGCAGGAA TTACCATTCT TCCTTTTGAT GAAAAAATC TAGACGGTGA 120
 TATGGAAATT ATCGCTGGAA ATGCCTTTTCG TCCAGATAAC AACGTCGAAA TTGCCTATGC 180
 GGACCAAAAT GGTATCAGCT ACAAACGTTA CCATGAGTTT CTAGGTAGCT TTATGCGTGA 240
 CTTTGTTAGC ATGGGAGTAG CAGGAGCACA TGGAAAAACT TCAACGACAG GTATGTTGTC 300
 TCATGTCTTG TCTCACATTA CAGATACCAG CTTCTTGATT GGAGATGGGA CAGGTCGTGG 360
 TTCGGCCAAT GCCAAATATT TTGTCTTTGA ATCTGACGAA TATGAGCGTC ACTTCATGCC 420
 TTACCACCCA GAATACTCTA TTATACCAA CATTGACTTT GACCATCCAG ATTATTTTAC 480
 AAGTCTCGAG GATGTTTMTA ATGCCTTTAA CGACTATGCC AAACAAATCA CCAAGGGTCT 540
 TTTTGTCTAT GGTGAAGATG CTGAATTGCG TAAGATTACG TCTGATGCAC CAATTTATTA 600
 TTATGGTTTT GAAGCTGAAG GCAATGACTT TGTAGCTAGT GATCTTCTTC GTTCAATAAC 660
 TGGTTCAACC TTCACCGTTC ATTTCCGTGG ACAAACCTTG GGGCAATTCC ACATTCCAAC 720
 CTTTGGTCGT CACAATATCA TGAATGCGAC AGCCGTTATT GGTCTTCTTT ACACAGCAGG 780
 ATTTGATTTG AACTTGGTGC GTGAGCACTT GAAAACATTT GCCGGTMTTA AACGTCGTTT 840
 CACTGAGAAA ATTGTCAATG ATACAGTGAT TATCGATGAC TTTGCCACC ATCCAACAGA 900
 AATTATTGCG ACCTTGGATG CGGCTCGTCA GAAATACCCA AGCAAGGAAA TTGTAGCAGT 960
 CTTTCAACCG CATACTTTA CAAGAACCAT TGCCTTGTG GACGACTTTG CCCATGCTTT 1020
 AAACCAAGCA GATGCTGTTT ATCTAGCGCA AATTATGGC TCGGCTCGTG AAGTAGATCA 1080
 TGGTGACGTT AAGGTAGAAG ACCTAGCCAA CAAAATCAAC AAAAAACACC AAGTGATTAC 1140
 TGTTGAAAAT GTTCTCCAC TCCTAGACCA TGACAATGCT GTTTACGTCT TTATGGGAGC 1200
 AGGAGACATC CAAACCTATG AATACTCATT TGAGCGTCTC TTGTCTAACT TGACAAGCAA 1260
 TGTTCAA 1267

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 422 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

His Gln Met Gly His Lys Val Gln Gly Ser Asp Val Glu Lys Tyr Tyr
 1 5 10 15

Phe Thr Gln Arg Gly Leu Glu Gln Ala Gly Ile Thr Ile Leu Pro Phe
 20 25 30
 Asp Glu Lys Asn Leu Asp Gly Asp Met Glu Ile Ile Ala Gly Asn Ala
 35 40 45
 Phe Arg Pro Asp Asn Asn Val Glu Ile Ala Tyr Ala Asp Gln Asn Gly
 50 55 60
 Ile Ser Tyr Lys Arg Tyr His Glu Phe Leu Gly Ser Phe Met Arg Asp
 65 70 75 80
 Phe Val Ser Met Gly Val Ala Gly Ala His Gly Lys Thr Ser Thr Thr
 85 90 95
 Gly Met Leu Ser His Val Leu Ser His Ile Thr Asp Thr Ser Phe Leu
 100 105 110
 Ile Gly Asp Gly Thr Gly Arg Gly Ser Ala Asn Ala Lys Tyr Phe Val
 115 120 125
 Phe Glu Ser Asp Glu Tyr Glu Arg His Phe Met Pro Tyr His Pro Glu
 130 135 140
 Tyr Ser Ile Ile Thr Asn Ile Asp Phe Asp His Pro Asp Tyr Phe Thr
 145 150 155 160
 Ser Leu Glu Asp Val Phe Asn Ala Phe Asn Asp Tyr Ala Lys Gln Ile
 165 170 175
 Thr Lys Gly Leu Phe Val Tyr Gly Glu Asp Ala Glu Leu Arg Lys Ile
 180 185 190
 Thr Ser Asp Ala Pro Ile Tyr Tyr Tyr Gly Phe Glu Ala Glu Gly Asn
 195 200 205
 Asp Phe Val Ala Ser Asp Leu Leu Arg Ser Ile Thr Gly Ser Thr Phe
 210 215 220
 Thr Val His Phe Arg Gly Gln Asn Leu Gly Gln Phe His Ile Pro Thr
 225 230 235 240
 Phe Gly Arg His Asn Ile Met Asn Ala Thr Ala Val Ile Gly Leu Leu
 245 250 255
 Tyr Thr Ala Gly Phe Asp Leu Asn Leu Val Arg Glu His Leu Lys Thr
 260 265 270
 Phe Ala Gly Val Lys Arg Arg Phe Thr Glu Lys Ile Val Asn Asp Thr
 275 280 285
 Val Ile Ile Asp Asp Phe Ala His His Pro Thr Glu Ile Ile Ala Thr
 290 295 300
 Leu Asp Ala Ala Arg Gln Lys Tyr Pro Ser Lys Glu Ile Val Ala Val
 305 310 315 320
 Phe Gln Pro His Thr Phe Thr Arg Thr Ile Ala Leu Leu Asp Asp Phe
 325 330 335
 Ala His Ala Leu Asn Gln Ala Asp Ala Val Tyr Leu Ala Gln Ile Tyr
 340 345 350

a'
 cont.

Gly Ser Ala Arg Glu Val Asp His Gly Asp Val Lys Val Glu Asp Leu
 355 360 365

Ala Asn Lys Ile Asn Lys Lys His Gln Val Ile Thr Val Glu Asn Val
 370 375 380

Ser Pro Leu Leu Asp His Asp Asn Ala Val Tyr Val Phe Met Gly Ala
 385 390 395 400

Gly Asp Ile Gln Thr Tyr Glu Tyr Ser Phe Glu Arg Leu Leu Ser Asn
 405 410 415

Leu Thr Ser Asn Val Gln
 420

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

TTTTAACCCA ACTGTGGTA CTTTCCTTTT TACTGCAGGA TTGAGCTTGT TAGTTTTATT 60

GGTTTCTAAA AGGGAAATG GAAAGAAACG ACTTGTTCAT TTTCTGCTGT TGACTAGCAT 120

GGGAGTTCAA TTGTTGCCGG CCAGTGCTTT TGGGTGACC AGCCAGATTT TATCTGCCTA 180

TAATAGTCAG CTTTCTATCG GAGTCGGGGA ACATTTACCA GAGCCTCTGA AAATCGAAGG 240

TTATCAATAT ATTGGTTATA TCAAACTAA GAAACAGGAT AATACAGAGC TTTCAAGGAC 300

AGTTGATGGG AAATACTCTG CTCAAAGAGA TAGTCAACCA AACTCTACAA AAACATCAGA 360

TGTAGTTCAT TCAGCTGATT TAGAATGGAA CCAAGGACAG GGAAGGTTA GTTTACAAGG 420

TGAAGCATCA GGGGATGATG GACTTTCAGA AAAATCTTCT ATAGCAGCAG ACAATCTATC 480

TTCTAATGAT TCATTGCGAA GTCAAGTTGA GCAGAATCCG GATCACAAAG GAGAATCTGT 540

AGTTTCACCA ACAGTGCCAG AACAAGGAAA TCCTGTGTCT GCTACAACGG TGCAGAGTGC 600

GGAAGAGGAA GTATTGGCGA CGACAAATGA TCGACCAGAG TATAAACTTC CATTTGGAAC 660

CAAAGGCACG CAAGAACCCG GTCATGAGGG TGAAGCCGCA GTCCGTGAAG ACTTACCACT 720

CTACACTAAG CCACTAGAAA CCAAAGGTAC ACAAGGACCC GGACATGAAG GTGAAGCTGC 780

AGTTTCGCGAG GAAGAACCAG CTTACACAGA ACCGTTAGCA ACGAAAGGCA CGCAAGAGCC 840

AGGTCATGAG GGCAAAGCTA CAGTCCGCGA AGAGACTCTA GAGTACACGG AACCGGTAGC 900

GACAAAAGGC ACACAAGAAC CCGAACATGA GGGCGAaCGG sCAGTAGAAG AAGAACTTCC 960

GGCTTTAGAG GTCACTACAC GAAATAGAAC GGAAATCCAG AATATTCCTT ATACAACAGA 1020

AGAAATTCAG GATCCAACAC TTCTGAAAAA TCGTCGTAAG ATTGAACGAC AAGGGCAAGC 1080

AGGGACACGT ACAATTCAAT ATGAAGACTA CATCGTAAAT GGTAATGTCG TAGAAACTAA 1140
 AGAAGTGTC ACGAAGTGAAG TAGCTCCGGT CAACGAAGTC GTTAAAGTAG GAACACTTGT 1200
 GAAAGTTAAA CCTACAGTAG AAATTACAAA CTTAACAAAA GTTGAGAACA AAAAATCTAT 1260
 AACTGTAAGT TATAACTTAA TAGACACTAC CTCAGCATAT GTTCTGCAA AAACGCAAGT 1320
 TTTCCATGGA GACAAGCTAG TTAAAGAGGT GGATATAGAA AATCCTGCCA AAGAGCAAGT 1380
 AATATCAGGT TTAGATTACT ACACACCGTA TACAGTTAAA ACACACCTAA CTTATAATTT 1440
 GGGTGAAAAT AATGAGGAAA ATACTGAAAC ATCAACTCAA GATTTCCAAT TAGAGTATAA 1500
 GAAAATAGAG ATTAAAGATA TTGATTCACT AGAATTATAC GGTAAGAAA ATGATCGTTA 1560
 TCGTAGATAT TTAAGTCTAA GTGAAGCGCC GACTGATACG GCTAAATACT TTGTAAAAGT 1620
 GAAATCAGAT CGCTTCAAAG AAATGTACCT ACCTGTAAAA TCTATTACAG AAAATACGGA 1680
 TGGAACGTAT AAAGTGACGG TAGCCGTTGA TCAACTTGTG GAAGAAGGTA CAGACGGTTA 1740
 CAAAGATGAT TACACATTTA CTGTAGCTAA ATCTAAAGCA GAGCAACCAG GAGTTTACAC 1800
 ATCCTTTAAA CAGCTGGTAA CAGCCATGCA AAGCAATCTG TCTGGTGTCT ATACATTGGC 1860
 TTCAGATATG ACCGCAGATG AGGTGAGCTT AGGCGATAAG CAGACAAGTT ATCTCACAGG 1920
 TGCATTTACA GGGAGCTTGA TCGGTTCTGA TGGAACAAAA TCGTATGCCA TTTATGATTT 1980
 GAAGAAACCA TTATTTGATA CATTAAATGG TGCTACAGTT AGAGATTTGG ATATTAAAC 2040
 TGTTTCTGCT GATAGTAAAG AAAATGTGCG AGCGCTGGCG AAGGCAGCGA ATAGCGCGAA 2100
 TATTAATAAT GTTGCAGTAG AAGGAAAAAT CTCAGGTGCG AAATCTGTTG CGGGATTAGT 2160
 AGCGAGCGCA ACAAATACAG TGATAGAAAA CAGCTCGTTT ACAGGGAAAC TTATCGCAAA 2220
 TCACCAGGAC AGTAATAAAA ATGATACTGG AGGAATAGTA GGTAATATAA CAGGAAATAG 2280
 TTCGAGAGTT AATAAAGTTA GGGTAGATGC CTTAATCTCT ACTAATGCAC GCAATAATAA 2340
 CCAAACAGCT GGAGGGATAG TAGGTAGATT AGAAAATGGT GCATTGATAT CTAATTCGGT 2400
 TGCTACTGGA GAAATACGAA ATGGTCAAGG ATATTTCTAGA GTCGGAGGAA TAGTAGGATC 2460
 TACGTGGCAA AACGGTCGAG TAAATAATGT TGTGAGTAAC GTAGATGTTG GAGATGGTTA 2520
 TGTTATCACC GGTGATCAAT ACGCAGCAGC AGATGTGAAA AATGCAAGTA CATCAGTTGA 2580
 TAATAGAAAA GCAGACAGAT TCGCTACAAA ATTATCAAAA GACCAAATAG ACGCGAAAGT 2640
 TGCTGATTAT GGAATCACAG TAACTCTTGA TGATACTGGG CAAGATTTAA AACGTAATCT 2700
 AAGAGAAGTT GATTATACAA GACTAAATAA AGCAGAAGCT GAAAGAAAAG TAGCTTATAG 2760
 CAACATAGAA AACTGATGC CATTTACAA TAAAGACCTA GTAGTTCACT ATGGTAACAA 2820
 AGTAGCGACA ACAGATAAAC TTTACACTAC AGAATTGTTA GATGTGTGTC CGATGAAAGA 2880
 TGATGAAGTA GTAACGGATA TTAATAATAA GAAAAATTCA ATAAATAAAG TTATGTTACA 2940
 TTTCAAAGAT AATACAGTAG AATACCTAGA TGTAACATTC AAAGAAAAC TCATAAACAG 3000

TCAAGTAATC GAATACAATG TTACAGGAAA AGAATATATA TTCACACCAG AAGCATTTGT 3060
 TTCAGACTAT ACAGCGATAA CGAATAACGT ACTAAGCGAC TTGCAAAATG TAACACTTAA 3120
 C 3121

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Phe Asn Pro Thr Val Gly Thr Phe Leu Phe Thr Ala Gly Leu Ser Leu
 1 5 10 15
 Leu Val Leu Leu Val Ser Lys Arg Glu Asn Gly Lys Lys Arg Leu Val
 20 25 30
 His Phe Leu Leu Leu Thr Ser Met Gly Val Gln Leu Leu Pro Ala Ser
 35 40 45
 Ala Phe Gly Leu Thr Ser Gln Ile Leu Ser Ala Tyr Asn Ser Gln Leu
 50 55 60
 Ser Ile Gly Val Gly Glu His Leu Pro Glu Pro Leu Lys Ile Glu Gly
 65 70 75 80
 Tyr Gln Tyr Ile Gly Tyr Ile Lys Thr Lys Lys Gln Asp Asn Thr Glu
 85 90 95
 Leu Ser Arg Thr Val Asp Gly Lys Tyr Ser Ala Gln Arg Asp Ser Gln
 100 105 110
 Pro Asn Ser Thr Lys Thr Ser Asp Val Val His Ser Ala Asp Leu Glu
 115 120 125
 Trp Asn Gln Gly Gln Gly Lys Val Ser Leu Gln Gly Glu Ala Ser Gly
 130 135 140
 Asp Asp Gly Leu Ser Glu Lys Ser Ser Ile Ala Ala Asp Asn Leu Ser
 145 150 155 160
 Ser Asn Asp Ser Phe Ala Ser Gln Val Glu Gln Asn Pro Asp His Lys
 165 170 175
 Gly Glu Ser Val Val Arg Pro Thr Val Pro Glu Gln Gly Asn Pro Val
 180 185 190
 Ser Ala Thr Thr Val Gln Ser Ala Glu Glu Glu Val Leu Ala Thr Thr
 195 200 205
 Asn Asp Arg Pro Glu Tyr Lys Leu Pro Leu Glu Thr Lys Gly Thr Gln
 210 215 220

Glu Pro Gly His Glu Gly Glu Ala Ala Val Arg Glu Asp Leu Pro Val
 225 230 235 240
 Tyr Thr Lys Pro Leu Glu Thr Lys Gly Thr Gln Gly Pro Gly His Glu
 245 250 255
 Gly Glu Ala Ala Val Arg Glu Glu Glu Pro Ala Tyr Thr Glu Pro Leu
 260 265 270
 Ala Thr Lys Gly Thr Gln Glu Pro Gly His Glu Gly Lys Ala Thr Val
 275 280 285
 Arg Glu Glu Thr Leu Glu Tyr Thr Glu Pro Val Ala Thr Lys Gly Thr
 290 295 300
 Gln Glu Pro Glu His Glu Gly Glu Arg Xaa Val Glu Glu Glu Leu Pro
 305 310 315 320
 Ala Leu Glu Val Thr Thr Arg Asn Arg Thr Glu Ile Gln Asn Ile Pro
 325 330 335
 Tyr Thr Thr Glu Glu Ile Gln Asp Pro Thr Leu Leu Lys Asn Arg Arg
 340 345 350
 Lys Ile Glu Arg Gln Gly Gln Ala Gly Thr Arg Thr Ile Gln Tyr Glu
 355 360 365
 Asp Tyr Ile Val Asn Gly Asn Val Val Glu Thr Lys Glu Val Ser Arg
 370 375 380
 Thr Glu Val Ala Pro Val Asn Glu Val Val Lys Val Gly Thr Leu Val
 385 390 395 400
 Lys Val Lys Pro Thr Val Glu Ile Thr Asn Leu Thr Lys Val Glu Asn
 405 410 415
 Lys Lys Ser Ile Thr Val Ser Tyr Asn Leu Ile Asp Thr Thr Ser Ala
 420 425 430
 Tyr Val Ser Ala Lys Thr Gln Val Phe His Gly Asp Lys Leu Val Lys
 435 440 445
 Glu Val Asp Ile Glu Asn Pro Ala Lys Glu Gln Val Ile Ser Gly Leu
 450 455 460
 Asp Tyr Tyr Thr Pro Tyr Thr Val Lys Thr His Leu Thr Tyr Asn Leu
 465 470 475 480
 Gly Glu Asn Asn Glu Glu Asn Thr Glu Thr Ser Thr Gln Asp Phe Gln
 485 490 495
 Leu Glu Tyr Lys Lys Ile Glu Ile Lys Asp Ile Asp Ser Val Glu Leu
 500 505 510
 Tyr Gly Lys Glu Asn Asp Arg Tyr Arg Arg Tyr Leu Ser Leu Ser Glu
 515 520 525
 Ala Pro Thr Asp Thr Ala Lys Tyr Phe Val Lys Val Lys Ser Asp Arg
 530 535 540
 Phe Lys Glu Met Tyr Leu Pro Val Lys Ser Ile Thr Glu Asn Thr Asp
 545 550 555 560

Gly Thr Tyr Lys Val Thr Val Ala Val Asp Gln Leu Val Glu Glu Gly
 565 570 575
 Thr Asp Gly Tyr Lys Asp Asp Tyr Thr Phe Thr Val Ala Lys Ser Lys
 580 585 590
 Ala Glu Gln Pro Gly Val Tyr Thr Ser Phe Lys Gln Leu Val Thr Ala
 595 600 605
 Met Gln Ser Asn Leu Ser Gly Val Tyr Thr Leu Ala Ser Asp Met Thr
 610 615 620
 Ala Asp Glu Val Ser Leu Gly Asp Lys Gln Thr Ser Tyr Leu Thr Gly
 625 630 635 640
 Ala Phe Thr Gly Ser Leu Ile Gly Ser Asp Gly Thr Lys Ser Tyr Ala
 645 650 655
 Ile Tyr Asp Leu Lys Lys Pro Leu Phe Asp Thr Leu Asn Gly Ala Thr
 660 665 670
 Val Arg Asp Leu Asp Ile Lys Thr Val Ser Ala Asp Ser Lys Glu Asn
 675 680 685
 Val Ala Ala Leu Ala Lys Ala Ala Asn Ser Ala Asn Ile Asn Asn Val
 690 695 700
 Ala Val Glu Gly Lys Ile Ser Gly Ala Lys Ser Val Ala Gly Leu Val
 705 710 715 720
 Ala Ser Ala Thr Asn Thr Val Ile Glu Asn Ser Ser Phe Thr Gly Lys
 725 730 735
 Leu Ile Ala Asn His Gln Asp Ser Asn Lys Asn Asp Thr Gly Gly Ile
 740 745 750
 Val Gly Asn Ile Thr Gly Asn Ser Ser Arg Val Asn Lys Val Arg Val
 755 760 765
 Asp Ala Leu Ile Ser Thr Asn Ala Arg Asn Asn Asn Gln Thr Ala Gly
 770 775 780
 Gly Ile Val Gly Arg Leu Glu Asn Gly Ala Leu Ile Ser Asn Ser Val
 785 790 795 800
 Ala Thr Gly Glu Ile Arg Asn Gly Gln Gly Tyr Ser Arg Val Gly Gly
 805 810 815
 Ile Val Gly Ser Thr Trp Gln Asn Gly Arg Val Asn Asn Val Val Ser
 820 825 830
 Asn Val Asp Val Gly Asp Gly Tyr Val Ile Thr Gly Asp Gln Tyr Ala
 835 840 845
 Ala Ala Asp Val Lys Asn Ala Ser Thr Ser Val Asp Asn Arg Lys Ala
 850 855 860
 Asp Arg Phe Ala Thr Lys Leu Ser Lys Asp Gln Ile Asp Ala Lys Val
 865 870 875 880
 Ala Asp Tyr Gly Ile Thr Val Thr Leu Asp Asp Thr Gly Gln Asp Leu
 885 890 895

Lys Arg Asn Leu Arg Glu Val Asp Tyr Thr Arg Leu Asn Lys Ala Glu
 900 905 910
 Ala Glu Arg Lys Val Ala Tyr Ser Asn Ile Glu Lys Leu Met Pro Phe
 915 920 925
 Tyr Asn Lys Asp Leu Val Val His Tyr Gly Asn Lys Val Ala Thr Thr
 930 935 940
 Asp Lys Leu Tyr Thr Thr Glu Leu Leu Asp Val Val Pro Met Lys Asp
 945 950 955 960
 Asp Glu Val Val Thr Asp Ile Asn Asn Lys Lys Asn Ser Ile Asn Lys
 965 970 975
 Val Met Leu His Phe Lys Asp Asn Thr Val Glu Tyr Leu Asp Val Thr
 980 985 990
 Phe Lys Glu Asn Phe Ile Asn Ser Gln Val Ile Glu Tyr Asn Val Thr
 995 1000 1005
 Gly Lys Glu Tyr Ile Phe Thr Pro Glu Ala Phe Val Ser Asp Tyr Thr
 1010 1015 1020
 Ala Ile Thr Asn Asn Val Leu Ser Asp Leu Gln Asn Val Thr Leu Asn
 1025 1030 1035 1040

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1567 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TTTTAACCCA ACTGTGGTA CTTTCCTTTT TACTGCAGGA TTGAGCTTGT TAGTTTTATT 60
 GGTTCCTAAA AGGGAAAATG GAAAGAAACG ACTTGTTTCAT TTTCTGCTGT TGACTAGCAT 120
 GGGAGTTCAA TTGTTGCCGG CCAGTGCTTT TGGGTGACC AGCCAGATT TATCTGCCTA 180
 TAATAGTCAG CTTTCTATCG GAGTCGGGA ACATTTACCA GAGCCTCTGA AAATCGAAGG 240
 TTATCAATAT ATTGGTTATA TCAAACTAA GAAACAGGAT AATACAGAGC TTTCAAGGAC 300
 AGTTGATGGG AAATACTCTG CTCAAAGAGA TAGTCAACCA AACTCTACAA AAACATCAGA 360
 TGTAAGTTCAT TCAGCTGATT TAGAATGGAA CCAAGGACAG GGAAGGTTA GTTTACAAGG 420
 TGAAGCATCA GGGGATGATG GACTTTCAGA AAAATCTTCT ATAGCAGCAG ACAATCTATC 480
 TTCTAATGAT TCATTGCGAA GTCAAGTTGA GCAGAATCCG GATCACAAAG GAGAATCTGT 540
 AGTTGACCA ACAGTGCCAG AACAAGGAAA TCCTGTGTCT GCTACAACGG TGCAGAGTGC 600
 GGAAGAGGAA GTATTGGCGA CGACAAATGA TCGACCAGAG TATAAACTTC CATTGGAAAC 660
 CAAAGGCACG CAAGAACCCG GTCATGAGGG TGAAGCCGCA GTCCGTGAAG ACTTACCACT 720

CTACACTAAG CCACTAGAAA CCAAAGGTAC ACAAGGACCC GGACATGAAG GTGAAGCTGC 780
 AGTTCGCGAG GAAGAACCAG CTTACACAGA ACCGTTAGCA ACGAAAGGCA CGCAAGAGCC 840
 AGGTCATGAG GGCAAAGCTA CAGTCCCGGA AGAGACTCTA GAGTACACGG AACCGGTAGC 900
 GACAAAAGGC ACACAAGAAC CCGAACATGA GGGCGAaCGG sCAGTAGAAG AAGAACTTCC 960
 GGCTTTTAGAG GTCACTACAC GAAATAGAAC GGAAATCCAG AATATTCTTT ATACAACAGA 1020
 AGAAATTCAG GATCCAACAC TTCTGAAAAA TCGTCGTAAG ATTGAACGAC AAGGGCAAGC 1080
 AGGGACACGT ACAATTCAAT ATGAAGACTA CATCGTAAAT GGTAATGTCG TAGAAACTAA 1140
 AGAAGTGTCA CGAACTGAAG TAGCTCCGGT CAACGAAGTC GTTAAAGTAG GAACACTTGT 1200
 GAAAGTTAAA CCTACAGTAG AAATTACAAA CTTAACAAAA GTTGAGAACA AAAAATCTAT 1260
 AACTGTAAGT TATAACTTAA TAGACACTAC CTCAGCATAT GTTTCGCAA AAACGCAAGT 1320
 TTTCCATGGA GACAAGCTAG TTAAAGAGGT GGATATAGAA AATCCTGCCA AAGAGCAAGT 1380
 AATATCAGGT TTAGATTACT ACACACCGTA TACAGTTAAA ACACACCTAA CTTATAATTT 1440
 GGGTGAAAAT AATGAGGAAA ATACTGAAAC ATCAACTCAA GATTTCCAAT TAGAGTATAA 1500
 GAAAATAGAG ATTAAAGATA TTGATTCAGT AGAATTATAC GGTAAGAAA ATGATCGTTA 1560
 TCGTAGA 1567

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 522 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Phe Asn Pro Thr Val Gly Thr Phe Leu Phe Thr Ala Gly Leu Ser Leu
 1 5 10 15
 Leu Val Leu Leu Val Ser Lys Arg Glu Asn Gly Lys Lys Arg Leu Val
 20 25 30
 His Phe Leu Leu Leu Thr Ser Met Gly Val Gln Leu Leu Pro Ala Ser
 35 40 45
 Ala Phe Gly Leu Thr Ser Gln Ile Leu Ser Ala Tyr Asn Ser Gln Leu
 50 55 60
 Ser Ile Gly Val Gly Glu His Leu Pro Glu Pro Leu Lys Ile Glu Gly
 65 70 75 80
 Tyr Gln Tyr Ile Gly Tyr Ile Lys Thr Lys Lys Gln Asp Asn Thr Glu
 85 90 95

Leu Ser Arg Thr Val Asp Gly Lys Tyr Ser Ala Gln Arg Asp Ser Gln
 100 105 110
 Pro Asn Ser Thr Lys Thr Ser Asp Val Val His Ser Ala Asp Leu Glu
 115 120 125
 Trp Asn Gln Gly Gln Gly Lys Val Ser Leu Gln Gly Glu Ala Ser Gly
 130 135 140
 Asp Asp Gly Leu Ser Glu Lys Ser Ser Ile Ala Ala Asp Asn Leu Ser
 145 150 155 160
 Ser Asn Asp Ser Phe Ala Ser Gln Val Glu Gln Asn Pro Asp His Lys
 165 170 175
 Gly Glu Ser Val Val Arg Pro Thr Val Pro Glu Gln Gly Asn Pro Val
 180 185 190
 Ser Ala Thr Thr Val Gln Ser Ala Glu Glu Glu Val Leu Ala Thr Thr
 195 200 205
 Asn Asp Arg Pro Glu Tyr Lys Leu Pro Leu Glu Thr Lys Gly Thr Gln
 210 215 220
 Glu Pro Gly His Glu Gly Glu Ala Ala Val Arg Glu Asp Leu Pro Val
 225 230 235 240
 Tyr Thr Lys Pro Leu Glu Thr Lys Gly Thr Gln Gly Pro Gly His Glu
 245 250 255
 Gly Glu Ala Ala Val Arg Glu Glu Glu Pro Ala Tyr Thr Glu Pro Leu
 260 265 270
 Ala Thr Lys Gly Thr Gln Glu Pro Gly His Glu Gly Lys Ala Thr Val
 275 280 285
 Arg Glu Glu Thr Leu Glu Tyr Thr Glu Pro Val Ala Thr Lys Gly Thr
 290 295 300
 Gln Glu Pro Glu His Glu Gly Glu Arg Xaa Val Glu Glu Glu Leu Pro
 305 310 315 320
 Ala Leu Glu Val Thr Thr Arg Asn Arg Thr Glu Ile Gln Asn Ile Pro
 325 330 335
 Tyr Thr Thr Glu Glu Ile Gln Asp Pro Thr Leu Leu Lys Asn Arg Arg
 340 345 350
 Lys Ile Glu Arg Gln Gly Gln Ala Gly Thr Arg Thr Ile Gln Tyr Glu
 355 360 365
 Asp Tyr Ile Val Asn Gly Asn Val Val Glu Thr Lys Glu Val Ser Arg
 370 375 380
 Thr Glu Val Ala Pro Val Asn Glu Val Val Lys Val Gly Thr Leu Val
 385 390 395 400
 Lys Val Lys Pro Thr Val Glu Ile Thr Asn Leu Thr Lys Val Glu Asn
 405 410 415
 Lys Lys Ser Ile Thr Val Ser Tyr Asn Leu Ile Asp Thr Thr Ser Ala
 420 425 430

Tyr Val Ser Ala Lys Thr Gln Val Phe His Gly Asp Lys Leu Val Lys
 435 440 445
 Glu Val Asp Ile Glu Asn Pro Ala Lys Glu Gln Val Ile Ser Gly Leu
 450 455 460
 Asp Tyr Tyr Thr Pro Tyr Thr Val Lys Thr His Leu Thr Tyr Asn Leu
 465 470 475 480
 Gly Glu Asn Asn Glu Glu Asn Thr Glu Thr Ser Thr Gln Asp Phe Gln
 485 490 495
 Leu Glu Tyr Lys Lys Ile Glu Ile Lys Asp Ile Asp Ser Val Glu Leu
 500 505 510
 Tyr Gly Lys Glu Asn Asp Arg Tyr Arg Arg
 515 520

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

TCGTAGATAT TTAAGTCTAA GTGAAGCGCC GACTGATACG GCTAAATACT TTGTAAAAGT 60
 GAAATCAGAT CGCTTCAAAG AAATGTACCT ACCTGTAAAA TCTATTACAG AAAATACGGA 120
 TGGAACGTAT AAAGTGACGG TAGCCGTGA TCAACTTGTC GAAGAAGGTA CAGACGGTTA 180
 CAAAGATGAT TACACATTTA CTGTAGCTAA ATCTAAAGCA GAGCAACCAG GAGTTTACAC 240
 ATCCTTTAAA CAGCTGGTAA CAGCCATGCA AAGCAATCTG TCTGGTGTCT ATACATTGGC 300
 TTCAGATATG ACCGCAGATG AGGTGAGCTT AGGCGATAAG CAGACAAGTT ATCTCACAGG 360
 TGCATTTACA GGGAGCTTGA TCGGTCTGA TGGAAACAAA TCGTATGCCA TTTATGATTT 420
 GAAGAAACCA TTATTTGATA CATTAAATGG TGCTACAGTT AGAGATTTGG ATATTAAAAC 480
 TGTTTCTGCT GATAGTAAAG AAAATGTCGC AGCGCTGGCG AAGGCAGCGA ATAGCGCGAA 540
 TATTAATAAT GTTGCAGTAG AAGGAAAAAT CTCAGGTGCG AAATCTGTTG CGGGATTAGT 600
 AGCGAGCGCA ACAAATACAG TGATAGAAAA CAGCTCGTTT ACAGGGAAAC TTATCGCAA 660
 TCACCAGGAC AGTAATAAAA ATGATACTGG AGGAATAGTA GGTAATATAA CAGGAAATAG 720
 TTCGAGAGTT AATAAAGTTA GGGTAGATGC CTTAATCTCT ACTAATGCAC GCAATAATAA 780
 CCAAACAGCT GGAGGGATAG TAGGTAGATT AGAAAATGGT GCATTGATAT CTAATTCGGT 840
 TGCTACTGGA GAAATACGAA ATGGTCAAGG ATATTCTAGA GTCGGAGGAA TAGTAGGATC 900
 TACGTGGCAA AACGGTCGAG TAAATAATGT TGTGAGTAAC GTAGATGTTG GAGATGGTTA 960

TGTATCACC GGTGATCAAT ACGCAGCAGC AGATGTGAAA AATGCAAGTA CATCAGTTGA 1020
 TAATAGAAAA GCAGACAGAT TCGCTACAAA ATTATCAAAA GACCAAATAG ACGCGAAAGT 1080
 TGCTGATTAT GGAATCACAG TAACTCTTGA TGATACTGGG CAAGATTTAA AACGTAATCT 1140
 AAGAGAAGTT GATTATACAA GACTAAATAA AGCAGAAGCT GAAAGAAAAG TAGCTTATAG 1200
 CAACATAGAA AAACGTATGC CATTCTACAA TAAAGACCTA GTAGTTCACAT ATGGTAACAA 1260
 AGTAGCGACA ACAGATAAAC TTTACACTAC AGAATTGTGA GATGTTGTGC CGATGAAAGA 1320
 TGATGAAGTA GTAACGGATA TTAATAATAA GAAAAATTCA ATAAATAAAG TTATGTTACA 1380
 TTCAAAGAT AATACAGTAG AATACCTAGA TGTAACATTC AAAGAAAAC TCATAAACAG 1440
 TCAAGTAATC GAATACAATG TTACAGGAAA AGAATATATA TTCACACCAG AAGCATTTGT 1500
 TTCAGACTAT ACAGCGATAA CGAATAACGT ACTAAGCGAC TTGCAAAATG TAACACTTAA 1560
 C 1561

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 520 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Arg Arg Tyr Leu Ser Leu Ser Glu Ala Pro Thr Asp Thr Ala Lys Tyr
 1 5 10 15
 Phe Val Lys Val Lys Ser Asp Arg Phe Lys Glu Met Tyr Leu Pro Val
 20 25 30
 Lys Ser Ile Thr Glu Asn Thr Asp Gly Thr Tyr Lys Val Thr Val Ala
 35 40 45
 Val Asp Gln Leu Val Glu Glu Gly Thr Asp Gly Tyr Lys Asp Asp Tyr
 50 55 60
 Thr Phe Thr Val Ala Lys Ser Lys Ala Glu Gln Pro Gly Val Tyr Thr
 65 70 75 80
 Ser Phe Lys Gln Leu Val Thr Ala Met Gln Ser Asn Leu Ser Gly Val
 85 90 95
 Tyr Thr Leu Ala Ser Asp Met Thr Ala Asp Glu Val Ser Leu Gly Asp
 100 105 110
 Lys Gln Thr Ser Tyr Leu Thr Gly Ala Phe Thr Gly Ser Leu Ile Gly
 115 120 125
 Ser Asp Gly Thr Lys Ser Tyr Ala Ile Tyr Asp Leu Lys Lys Pro Leu
 130 135 140

Phe Asp Thr Leu Asn Gly Ala Thr Val Arg Asp Leu Asp Ile Lys Thr
 145 150 155 160
 Val Ser Ala Asp Ser Lys Glu Asn Val Ala Ala Leu Ala Lys Ala Ala
 165 170 175
 Asn Ser Ala Asn Ile Asn Asn Val Ala Val Glu Gly Lys Ile Ser Gly
 180 185 190
 Ala Lys Ser Val Ala Gly Leu Val Ala Ser Ala Thr Asn Thr Val Ile
 195 200 205
 Glu Asn Ser Ser Phe Thr Gly Lys Leu Ile Ala Asn His Gln Asp Ser
 210 215 220
 Asn Lys Asn Asp Thr Gly Gly Ile Val Gly Asn Ile Thr Gly Asn Ser
 225 230 235 240
 Ser Arg Val Asn Lys Val Arg Val Asp Ala Leu Ile Ser Thr Asn Ala
 245 250 255
 Arg Asn Asn Asn Gln Thr Ala Gly Gly Ile Val Gly Arg Leu Glu Asn
 260 265 270
 Gly Ala Leu Ile Ser Asn Ser Val Ala Thr Gly Glu Ile Arg Asn Gly
 275 280 285
 Gln Gly Tyr Ser Arg Val Gly Gly Ile Val Gly Ser Thr Trp Gln Asn
 290 295 300
 Gly Arg Val Asn Asn Val Val Ser Asn Val Asp Val Gly Asp Gly Tyr
 305 310 315 320
 Val Ile Thr Gly Asp Gln Tyr Ala Ala Ala Asp Val Lys Asn Ala Ser
 325 330 335
 Thr Ser Val Asp Asn Arg Lys Ala Asp Arg Phe Ala Thr Lys Leu Ser
 340 345 350
 Lys Asp Gln Ile Asp Ala Lys Val Ala Asp Tyr Gly Ile Thr Val Thr
 355 360 365
 Leu Asp Asp Thr Gly Gln Asp Leu Lys Arg Asn Leu Arg Glu Val Asp
 370 375 380
 Tyr Thr Arg Leu Asn Lys Ala Glu Ala Glu Arg Lys Val Ala Tyr Ser
 385 390 395 400
 Asn Ile Glu Lys Leu Met Pro Phe Tyr Asn Lys Asp Leu Val Val His
 405 410 415
 Tyr Gly Asn Lys Val Ala Thr Thr Asp Lys Leu Tyr Thr Thr Glu Leu
 420 425 430
 Leu Asp Val Val Pro Met Lys Asp Asp Glu Val Val Thr Asp Ile Asn
 435 440 445
 Asn Lys Lys Asn Ser Ile Asn Lys Val Met Leu His Phe Lys Asp Asn
 450 455 460
 Thr Val Glu Tyr Leu Asp Val Thr Phe Lys Glu Asn Phe Ile Asn Ser
 465 470 475 480

Gln Val Ile Glu Tyr Asn Val Thr Gly Lys Glu Tyr Ile Phe Thr Pro
 485 490 495

Glu Ala Phe Val Ser Asp Tyr Thr Ala Ile Thr Asn Asn Val Leu Ser
 500 505 510

Asp Leu Gln Asn Val Thr Leu Asn
 515 520

(2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 850 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

CTTTGGTTT GAAGGAAGTA AGCGTGGACA ATTGCTGTGA GAAGGAATCA ATCAACTTCG 60
 TGAGCATGTA GACACTCTAT TGATTATCTC AAACAACAAT TTGCTTGAAA TTGTTGATAA 120
 GAAAACACCG CTTTGGAGG CTCTTAGCGA AGCGGATAAC GTTCTTCGTC AAGGTGTTCA 180
 AGGGATTACC GATTTGATTA CCAATCCAGG ATTGATTAAC CTTGACTTTG CCGATGTGAA 240
 AACGGTAATG GCAAACAAAG GGAATGCTCT TATGGGTATT GGTATCGGTA GTGGAGAAGA 300
 ACGTGTGGTA GAAGCGGCAC GTAAGGCAAT CTATTCACCA CTTCTTGAAA CAACTATTGA 360
 CGGTGCTGAG GATGTTATCG TCAACGTTAC TGGTGGTCTT GACTTAACCT TGATTGAGGC 420
 AGAAGAGGCT TCACAAATTG TGAACCAGGC AGCAGGTCAA GGAGTGAACA TCTGGCTCGG 480
 TACTTCAATT GATGAAAGTA TCGTGATGA AATTCGTGTA ACAGTTGTTG CAACGGGTGT 540
 TCGTCAAGAC CGCGTAGAAA AGGTTGTGGC TCCACAAGCT AGATCTGCTA CTAAC TACCG 600
 TGAGACAGTG AAACCAGCTC ATTCACATGG CTTTGATCGT CATTTTGATA TGGCAGAAAC 660
 AGTTGAATTG CAAAAACAAA ATCCACGTCG TTTGGAACCA ACTCAGGCAT CTGCTTTTGG 720
 TGATTGGGAT CTTGCCGTG AATCGATTGT TCGTACAACA GATTCACTCG TTTCTCCAGT 780
 CGAGCGCTTT GAAGCCCCAA TTTCACAAGA TGAAGATGAA TTGGATACAC CTCCATTTT 840
 CAAAAATCGT 850

(2) INFORMATION FOR SEQ ID NO: 124:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 283 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Phe Gly Phe Glu Gly Ser Lys Arg Gly Gln Phe Ala Val Glu Gly Ile
 1 5 10 15
 Asn Gln Leu Arg Glu His Val Asp Thr Leu Leu Ile Ile Ser Asn Asn
 20 25 30
 Asn Leu Leu Glu Ile Val Asp Lys Lys Thr Pro Leu Leu Glu Ala Leu
 35 40 45
 Ser Glu Ala Asp Asn Val Leu Arg Gln Gly Val Gln Gly Ile Thr Asp
 50 55 60
 Leu Ile Thr Asn Pro Gly Leu Ile Asn Leu Asp Phe Ala Asp Val Lys
 65 70 75 80
 Thr Val Met Ala Asn Lys Gly Asn Ala Leu Met Gly Ile Gly Ile Gly
 85 90 95
 Ser Gly Glu Glu Arg Val Val Glu Ala Ala Arg Lys Ala Ile Tyr Ser
 100 105 110
 Pro Leu Leu Glu Thr Thr Ile Asp Gly Ala Glu Asp Val Ile Val Asn
 115 120 125
 Val Thr Gly Gly Leu Asp Leu Thr Leu Ile Glu Ala Glu Glu Ala Ser
 130 135 140
 Gln Ile Val Asn Gln Ala Ala Gly Gln Gly Val Asn Ile Trp Leu Gly
 145 150 155 160
 Thr Ser Ile Asp Glu Ser Met Arg Asp Glu Ile Arg Val Thr Val Val
 165 170 175
 Ala Thr Gly Val Arg Gln Asp Arg Val Glu Lys Val Val Ala Pro Gln
 180 185 190
 Ala Arg Ser Ala Thr Asn Tyr Arg Glu Thr Val Lys Pro Ala His Ser
 195 200 205
 His Gly Phe Asp Arg His Phe Asp Met Ala Glu Thr Val Glu Leu Pro
 210 215 220
 Lys Gln Asn Pro Arg Arg Leu Glu Pro Thr Gln Ala Ser Ala Phe Gly
 225 230 235 240
 Asp Trp Asp Leu Arg Arg Glu Ser Ile Val Arg Thr Thr Asp Ser Val
 245 250 255
 Val Ser Pro Val Glu Arg Phe Glu Ala Pro Ile Ser Gln Asp Glu Asp
 260 265 270
 Glu Leu Asp Thr Pro Pro Phe Phe Lys Asn Arg
 275 280

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1051 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

CTACTACCTC TCGAGAGAAA GTGACCTAGA GGTGACCGTT TTTGACCATG AGCAAGGTCA 60
AGCCACCAAG GCCGCAGCAG GAATTATCAG TCCTTGGTTT TCCAAACGCC GTAATAAAGC 120
CTGGTACAAG ATGGCGCGCT TGGGGGCTGA TTTTATGTG GATTTATTAG CTGATTTAGA 180
GAAATCAGGA CAAGAAATCG ACTTTTACCA GCGTTCGGGA GTCTTTCTCT TGAAAAAGGA 240
TGAATCCAAT TTGGAAGAAC TTTATCAACT GGCCCTCCAG CGCAGAGAAG AATCTCCCTT 300
GATAGGGCAA TTAGCCATTC TGAACCAAGC CTCAGCTAAT GAATTATTC CTGGTTTGCA 360
GGGATTTGAC CGCCTGCTCT ATGCTTCTGG TGGAGCGAGA GTAGATGGCC AACTTTTAGT 420
GACTCGTTTG CTGGAAGTCA GTCATGTCAA GCTGGTCAA GAAAAAGTGA CTCTGACACC 480
GTTAGCATCA GGCTACCAGA TTGGTGAAGA GGAGTTTGAG CAGGTTATTT TGGCGACGGG 540
AGCTTGGTGT GGGGACATGT TAGAGCCTTT AGGTATGAA GTGGATGTCC GTCCTCAAAA 600
AGGACAATA CGAGATTATC AGCTTGCCCA AGACATGGAA GATTACCCTG TTGTCATGCC 660
AGAAGGGGAG TGGGATTTGA TTCCCTTTGC AGGTGGGAAA TTATCCTTAG GCGCTACCCA 720
CGAAAATGAC ATGGGATTTG ATTTGACGGT AGATGAAACC TTGCTCCAAC AAATGGAGGA 780
GGCCACCTTG ACTCACTATC TGATTTTGGC TGAAGCTACT TCAAAATCTG AGCGTGTGG 840
AATCCGTGCC TACACCAGTG ATTTCTCTCC TTTCTTTGGG CAGGTGCCTG ACTTAACTGG 900
TGTCTATGCA GCCAGTGGAC TAGGTTTCATC AGGCTCACA ACTGGTCCTA TCATTGGTTA 960
CCATCTAGCC CAACTGATCC AAGACAAGGA GTTGACCTTG GACCCCTCTAA ATTACCCAAT 1020
TGAAAACATAT GTCAAACGAG TAAAAGCGA A 1051

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 350 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Tyr Tyr Leu Ser Arg Glu Ser Asp Leu Glu Val Thr Val Phe Asp His
1 5 10 15
Glu Gln Gly Gln Ala Thr Lys Ala Ala Ala Gly Ile Ile Ser Pro Trp
20 25 30

Phe Ser Lys Arg Arg Asn Lys Ala Trp Tyr Lys Met Ala Arg Leu Gly
 35 40 45
 Ala Asp Phe Tyr Val Asp Leu Leu Ala Asp Leu Glu Lys Ser Gly Gln
 50 55 60
 Glu Ile Asp Phe Tyr Gln Arg Ser Gly Val Phe Leu Leu Lys Lys Asp
 65 70 75 80
 Glu Ser Asn Leu Glu Glu Leu Tyr Gln Leu Ala Leu Gln Arg Arg Glu
 85 90 95
 Glu Ser Pro Leu Ile Gly Gln Leu Ala Ile Leu Asn Gln Ala Ser Ala
 100 105 110
 Asn Glu Leu Phe Pro Gly Leu Gln Gly Phe Asp Arg Leu Leu Tyr Ala
 115 120 125
 Ser Gly Gly Ala Arg Val Asp Gly Gln Leu Leu Val Thr Arg Leu Leu
 130 135 140
 Glu Val Ser His Val Lys Leu Val Lys Glu Lys Val Thr Leu Thr Pro
 145 150 155 160
 Leu Ala Ser Gly Tyr Gln Ile Gly Glu Glu Glu Phe Glu Gln Val Ile
 165 170 175
 Leu Ala Thr Gly Ala Trp Leu Gly Asp Met Leu Glu Pro Leu Gly Tyr
 180 185 190
 Glu Val Asp Val Arg Pro Gln Lys Gly Gln Leu Arg Asp Tyr Gln Leu
 195 200 205
 Ala Gln Asp Met Glu Asp Tyr Pro Val Val Met Pro Glu Gly Glu Trp
 210 215 220
 Asp Leu Ile Pro Phe Ala Gly Gly Lys Leu Ser Leu Gly Ala Thr His
 225 230 235 240
 Glu Asn Asp Met Gly Phe Asp Leu Thr Val Asp Glu Thr Leu Leu Gln
 245 250 255
 Gln Met Glu Glu Ala Thr Leu Thr His Tyr Leu Ile Leu Ala Glu Ala
 260 265 270
 Thr Ser Lys Ser Glu Arg Val Gly Ile Arg Ala Tyr Thr Ser Asp Phe
 275 280 285
 Ser Pro Phe Phe Gly Gln Val Pro Asp Leu Thr Gly Val Tyr Ala Ala
 290 295 300
 Ser Gly Leu Gly Ser Ser Gly Leu Thr Thr Gly Pro Ile Ile Gly Tyr
 305 310 315 320
 His Leu Ala Gln Leu Ile Gln Asp Lys Glu Leu Thr Leu Asp Pro Leu
 325 330 335
 Asn Tyr Pro Ile Glu Asn Tyr Val Lys Arg Val Lys Ser Glu
 340 345 350

(2) INFORMATION FOR SEQ ID NO: 127:

244

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

TAAGGTCAAA AGTCAGACCG CTAAGAAAGT GCTAGAAAAG ATTGGAGCTG ACTCGGTTAT	60
CTCGCCAGAG TATGAAATGG GGCAGTCTCT AGCACAGACC ATTCTTTTCC ATAATAGTGT	120
TGATGTCTTT CAGTTGGATA AAAATGTGTC TATCGTGGAG ATGAAAATTC CTCAGTCTTG	180
GGCAGGTCAA AGTCTGAGTA AATTAGACCT CCGTGGCAAA TACAATCTGA ATATTTTGGG	240
TTTCCGAGAG CAGGAAAATT CCCCATTTGA TGTGAATTT GGACCAGATG ACCTCTTGAA	300
AGCAGATACC TATATTTTGG CAGTCATCAA CAACCAGTAT TTGGATACCC TA	352

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Lys Val Lys Ser Gln Thr Ala Lys Lys Val Leu Glu Lys Ile Gly Ala	1	5	10	15
Asp Ser Val Ile Ser Pro Glu Tyr Glu Met Gly Gln Ser Leu Ala Gln	20	25	30	
Thr Ile Leu Phe His Asn Ser Val Asp Val Phe Gln Leu Asp Lys Asn	35	40	45	
Val Ser Ile Val Glu Met Lys Ile Pro Gln Ser Trp Ala Gly Gln Ser	50	55	60	
Leu Ser Lys Leu Asp Leu Arg Gly Lys Tyr Asn Leu Asn Ile Leu Gly	65	70	75	80
Phe Arg Glu Gln Glu Asn Ser Pro Leu Asp Val Glu Phe Gly Pro Asp	85	90	95	
Asp Leu Leu Lys Ala Asp Thr Tyr Ile Leu Ala Val Ile Asn Asn Gln	100	105	110	
Tyr Leu Asp Thr Leu	115			

(2) INFORMATION FOR SEQ ID NO: 129:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 247 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

TGACGGGTCT CAGGATCAGA CTCAGGAAAT CGCTGAGTGT TTAGCTAGCA AGTATCCTAA	60
TATCGTTAGA GCCATCTATC AGGAAAATAA ATGCCATGGC GGTGCGGTCA ATCGTGGCTT	120
GGTAGAGGCT TCTGGGCGCT ATTTTAAAGT AGTTGACAGT GATGACTGGG TGGATCCTCG	180
TGCCTACTTG AAAATTCTTG AAACTTGCAG GAACTTGAGA GCAAAGGTCA AGAGGTGGAT	240
GTCTTTG	247

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 82 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Gly Ser Gln Asp Gln Thr Gln Glu Ile Ala Glu Cys Leu Ala Ser	
1 5 10 15	
Lys Tyr Pro Asn Ile Val Arg Ala Ile Tyr Gln Glu Asn Lys Cys His	
20 25 30	
Gly Gly Ala Val Asn Arg Gly Leu Val Glu Ala Ser Gly Arg Tyr Phe	
35 40 45	
Lys Val Val Asp Ser Asp Asp Trp Val Asp Pro Arg Ala Tyr Leu Lys	
50 55 60	
Ile Leu Glu Thr Cys Arg Asn Leu Arg Ala Lys Val Lys Arg Trp Met	
65 70 75 80	
Ser Leu	

(2) INFORMATION FOR SEQ ID NO: 131:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1744 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

TAGAGGCTTT GCCAAATGGT GGAAGGGCA CGAGCGTCGA AAAGAGGAAC GCTTTGTCAA 60
 ACAAGAAGAA AAAGCTCGCC AAAAGGCTGA GAAAGAGGCT AGATTAGAAC AAGAAGAGAC 120
 TGAAAAAGCC TTAAGCTGATT TGCCTCCTGT TGATATGGAA ACGGGTGAAA TTCTGACAGA 180
 GGAAGCTGTT CAAATCTTC CACCTATTCC AGAAGAAAAG TGGGTGGAAC CAGAAATCAT 240
 CCTGCCTCAA GCTGAACTTA AATTCCCTGA ACAGGAAGAT GACTCAGATG ACGAAGATGT 300
 TCAGGTCGAT TTTTCAGCCA AAGAAGCCCT TGAATACAAA CTTCCAAGCT TACAACCTTT 360
 TGCACCAGAT AAACCAAAAG ATCAGTCTAA AGAGAAGAAA ATTGTCTAGAG AAAATATCAA 420
 AATCTTAGAA GCAACCTTTG CTAGCTTTGG TATTAAGGTA ACAGTTGAAC GGGCCGAAAT 480
 TGGGCCATCA GTGACCAAGT ATGAAGTCAA GCCGCTGTT GGTGTAAGGG TCAACCGCAT 540
 TTCCAATCTA TCAGATGACC TCGCTCTAGC CTTGGCTGCC AAAGATGTCC GGATTGAAGC 600
 ACCAATCCCT GGGAAATCCC TAATCGGAAT TGAAGTGCCC AACTCCGATA TTGCCACTGT 660
 ATCTTTCCGA GAACTATGGG AACAAATCGCA AACGAAAGCA GAAATTTCT TGGAAATTC 720
 TTTAGGAAG GCTGTTAATG GAACCGCAAG AGCTTTTGAC CTTCTAAAA TGCCCCACTT 780
 GCTAGTTGCA GGTCAACGG GTTCAGGGA GTCAGTAGCA GTTAACGGCA TTATTGCTAG 840
 CATTCTCATG AAGCGAGAC CAGATCAAGT TAAATTTATG ATGGTCGATC CCAAGATGGT 900
 TGAGTTATCT GTTTACAATG ATATTCCCCA CCTCTTGATT CCAGTCGTGA CCAATCCACG 960
 CAAAGCCAGC AAGGCTCTGC AAAAGGTTGT GGATGAAATG GAAAACCGTT ATGAACTCTT 1020
 TGCCAAGGTG GGAGTTCCGA ATATTGCAGG TTTAATGCC AAGGTAGAAG AGTTCAATTC 1080
 CCAGTCTGAG TACAAGCAAA TTCCGCTACC ATTCATTGTC GTGATTGTGG ATGAGTTGGC 1140
 TGACCTCATG ATGGTGGCCA GCAAGGAAGT GGAAGATGCT ATCATCCGTC TTGGGCAGAA 1200
 GCGCGTGCT GCAGGTATCC ACATGATCTT TGCAACTCAG CGTCCATCTG TTGATGTCAT 1260
 CTCTGGTTTG ATTAAGGCCA ATGTTCCATC TCGTGTAGCA TTTGCGGTTT CATCAGGAAC 1320
 AGACTCCCGT ACGATTTTGG ATGAAAATGG AGCAGAAAAA CTTCTTGGTC GAGGAGACAT 1380
 GCTCTTTAAA CCGATTGATG AAAATCATCC AGTTCGTCTC CAAGGCTCCT TTATCTCGGA 1440
 TGACGATGTT GAGCGCATTG TGAACATCAT CAAGACTCAG GCAGATGCAG ACTACGATGA 1500
 GAGTTTGTAT CCAGGTGAGG TTTCTGAAAA TGAAGGAGAA TTTTCGGATG GAGATGCTGG 1560
 TGGTGATCCG CTTTGTGAAG AAGCTAAGTC TTTGGTTATC GAAACACAGA AAGCCAGTGC 1620
 GTCTATGATT CAGCGTCGTT TATCAGTTGG ATTTAACCGT GCGACCCGTC TCATGGAAGA 1680
 ACTGGAGATA GCAGGTGTCA TCGGTCCAGC TGAAGGTACC AAACCTCGAA AAGTGTTACA 1740
 ACAA 1744

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 581 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Arg Gly Phe Ala Lys Trp Trp Glu Gly His Glu Arg Arg Lys Glu Glu
 1 5 10 15
 Arg Phe Val Lys Gln Glu Glu Lys Ala Arg Gln Lys Ala Glu Lys Glu
 20 25 30
 Ala Arg Leu Glu Gln Glu Glu Thr Glu Lys Ala Leu Leu Asp Leu Pro
 35 40 45
 Pro Val Asp Met Glu Thr Gly Glu Ile Leu Thr Glu Glu Ala Val Gln
 50 55 60
 Asn Leu Pro Pro Ile Pro Glu Glu Lys Trp Val Glu Pro Glu Ile Ile
 65 70 75 80
 Leu Pro Gln Ala Glu Leu Lys Phe Pro Glu Gln Glu Asp Asp Ser Asp
 85 90 95
 Asp Glu Asp Val Gln Val Asp Phe Ser Ala Lys Glu Ala Leu Glu Tyr
 100 105 110
 Lys Leu Pro Ser Leu Gln Leu Phe Ala Pro Asp Lys Pro Lys Asp Gln
 115 120 125
 Ser Lys Glu Lys Lys Ile Val Arg Glu Asn Ile Lys Ile Leu Glu Ala
 130 135 140
 Thr Phe Ala Ser Phe Gly Ile Lys Val Thr Val Glu Arg Ala Glu Ile
 145 150 155 160
 Gly Pro Ser Val Thr Lys Tyr Glu Val Lys Pro Ala Val Gly Val Arg
 165 170 175
 Val Asn Arg Ile Ser Asn Leu Ser Asp Asp Leu Ala Leu Ala Leu Ala
 180 185 190
 Ala Lys Asp Val Arg Ile Glu Ala Pro Ile Pro Gly Lys Ser Leu Ile
 195 200 205
 Gly Ile Glu Val Pro Asn Ser Asp Ile Ala Thr Val Ser Phe Arg Glu
 210 215 220
 Leu Trp Glu Gln Ser Gln Thr Lys Ala Glu Asn Phe Leu Glu Ile Pro
 225 230 235 240
 Leu Gly Lys Ala Val Asn Gly Thr Ala Arg Ala Phe Asp Leu Ser Lys
 245 250 255
 Met Pro His Leu Leu Val Ala Gly Ser Thr Gly Ser Gly Lys Ser Val

260 265 270

Ala Val Asn Gly Ile Ile Ala Ser Ile Leu Met Lys Ala Arg Pro Asp
275 280 285

Gln Val Lys Phe Met Met Val Asp Pro Lys Met Val Glu Leu Ser Val
290 295 300

Tyr Asn Asp Ile Pro His Leu Leu Ile Pro Val Val Thr Asn Pro Arg
305 310 315 320

Lys Ala Ser Lys Ala Leu Gln Lys Val Val Asp Glu Met Glu Asn Arg
325 330 335

Tyr Glu Leu Phe Ala Lys Val Gly Val Arg Asn Ile Ala Gly Phe Asn
340 345 350

Ala Lys Val Glu Glu Phe Asn Ser Gln Ser Glu Tyr Lys Gln Ile Pro
355 360 365

Leu Pro Phe Ile Val Val Ile Val Asp Glu Leu Ala Asp Leu Met Met
370 375 380

Val Ala Ser Lys Glu Val Glu Asp Ala Ile Ile Arg Leu Gly Gln Lys
385 390 395 400

Ala Arg Ala Ala Gly Ile His Met Ile Leu Ala Thr Gln Arg Pro Ser
405 410 415

Val Asp Val Ile Ser Gly Leu Ile Lys Ala Asn Val Pro Ser Arg Val
420 425 430

Ala Phe Ala Val Ser Ser Gly Thr Asp Ser Arg Thr Ile Leu Asp Glu
435 440 445

Asn Gly Ala Glu Lys Leu Leu Gly Arg Gly Asp Met Leu Phe Lys Pro
450 455 460

Ile Asp Glu Asn His Pro Val Arg Leu Gln Gly Ser Phe Ile Ser Asp
465 470 475 480

Asp Asp Val Glu Arg Ile Val Asn Phe Ile Lys Thr Gln Ala Asp Ala
485 490 495

Asp Tyr Asp Glu Ser Phe Asp Pro Gly Glu Val Ser Glu Asn Glu Gly
500 505 510

Glu Phe Ser Asp Gly Asp Ala Gly Gly Asp Pro Leu Phe Glu Glu Ala
515 520 525

Lys Ser Leu Val Ile Glu Thr Gln Lys Ala Ser Ala Ser Met Ile Gln
530 535 540

Arg Arg Leu Ser Val Gly Phe Asn Arg Ala Thr Arg Leu Met Glu Glu
545 550 555 560

Leu Glu Ile Ala Gly Val Ile Gly Pro Ala Glu Gly Thr Lys Pro Arg
565 570 575

Lys Val Leu Gln Gln
580

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

TCAAAAAGAG AAGGAAAAC TGGTTATTGC TGGGAAAATA GGTCCAGAAC CAGAAATTTT 60
 GGCCAATATG TATAAGTTGC TGATTGAAGA AAATACCAGC ATGACTGCGA CTGTTAAACC 120
 GAATTTTGGG AAGACAAGCT TCCTTTATGA AGCTCTGAAA AAAGGCGATA TTGACATCTA 180
 TCCTGAATTT ACTGGTACGG TGA CTGAAAAG TTTGCTTCAA CCATCACCCA AGGTGAGTCA 240
 TGAACCAGAA CAGGTTTATC AGGTGGCGCG TGATGGCATT GCTAAGCAGG ATCATCTAGC 300
 CTATCTCAAA CCCATGTCTT ATCAAAACAC CTATGCTGTA GCTGTTCCGA AAAAGATTGC 360
 TCAAGAATAT GGCTTGAAGA CCATTTTCTA CTGAAAAA GTGGAAGGGC AGTTGAAGGC 420
 AGGTTTTACA CTCGAGTTTA ACGACCGTGA AGATGGAAAT AAGGGCTTGC AATCAATGTA 480
 TGGTCTCAAT CTCAATGTAG CGACCATTTGA GCCAGCCCTT CGCTATCAGG CTATTCAGTC 540
 AGGGGATATT CAAATCACGG ATGCCTATTC GACTGATGCG GAATTGGAGC GTTATGATTT 600
 ACAGGTCTTG GAAGATGACA AGCAACTCTT CCCACCTTAT CAAGGGGCTC CACTCATGAA 660
 AGAAGCTCTT CTCAAGAAAC ACCCAGAGTT GGAAAGAGTT CTTAATACAT TGGCTGGTAA 720
 GATTACAGAA AGCCAGATGA GCCAGCTCAA CTACCAAGTC GGTGTTGAAG GCAAGTCAGC 780
 AAAGCAAGTA GCCAAGGAGT TTCTCCAAGA ACAAGGTTTG TTGAAGAAA 829

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Gln Lys Glu Lys Glu Asn Leu Val Ile Ala Gly Lys Ile Gly Pro Glu
 1 5 10 15
 Pro Glu Ile Leu Ala Asn Met Tyr Lys Leu Leu Ile Glu Glu Asn Thr
 20 25 30
 Ser Met Thr Ala Thr Val Lys Pro Asn Phe Gly Lys Thr Ser Phe Leu
 35 40 45

Tyr Glu Ala Leu Lys Lys Gly Asp Ile Asp Ile Tyr Pro Glu Phe Thr
 50 55 60
 Gly Thr Val Thr Glu Ser Leu Leu Gln Pro Ser Pro Lys Val Ser His
 65 70 75 80
 Glu Pro Glu Gln Val Tyr Gln Val Ala Arg Asp Gly Ile Ala Lys Gln
 85 90 95
 Asp His Leu Ala Tyr Leu Lys Pro Met Ser Tyr Gln Asn Thr Tyr Ala
 100 105 110
 Val Ala Val Pro Lys Lys Ile Ala Gln Glu Tyr Gly Leu Lys Thr Ile
 115 120 125
 Ser Asp Leu Lys Lys Val Glu Gly Gln Leu Lys Ala Gly Phe Thr Leu
 130 135 140
 Glu Phe Asn Asp Arg Glu Asp Gly Asn Lys Gly Leu Gln Ser Met Tyr
 145 150 155 160
 Gly Leu Asn Leu Asn Val Ala Thr Ile Glu Pro Ala Leu Arg Tyr Gln
 165 170 175
 Ala Ile Gln Ser Gly Asp Ile Gln Ile Thr Asp Ala Tyr Ser Thr Asp
 180 185 190
 Ala Glu Leu Glu Arg Tyr Asp Leu Gln Val Leu Glu Asp Asp Lys Gln
 195 200 205
 Leu Phe Pro Pro Tyr Gln Gly Ala Pro Leu Met Lys Glu Ala Leu Leu
 210 215 220
 Lys Lys His Pro Glu Leu Arg Val Leu Asn Thr Leu Ala Gly Lys
 225 230 235 240
 Ile Thr Glu Ser Gln Met Ser Gln Leu Asn Tyr Gln Val Gly Val Glu
 245 250 255
 Gly Lys Ser Ala Lys Gln Val Ala Lys Glu Phe Leu Gln Glu Gln Gly
 260 265 270
 Leu Leu Lys Lys
 275

(2) INFORMATION FOR SEQ ID NO: 135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 712 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

ACGTTCTATT GAGGACCACT TTGATTCAAA CTTGGAATTG GAATATAACC TCAAAGAAAA	60
AGGGAAAACA GATCTTTTGA AGCTAGTTGA TAAACAACCT GACATGCGTC TGCATTTTAT	120
CCGCCAACT CATCCACGCG GTCTCGGAGA TGCTGTTTTG CAAGCCAAGG CTTTCGTCGG	180

AAATGAACCT TTTGTCGTTA TGCTTGGTGA TGAATTGATG GATATCACAG ACGAAAAGGC 240
 TGTTCACACTT ACCAAACAAC TCATGGATGA CTACGAGCGT ACCCAGCGGT CTACTATCGC 300
 TGTCATGCCA GTCCCTCATG ACGAAGTATC TGCTTACGGG GTTATTGCTC CGCAAGGCCA 360
 AGGAAAAGAT GGTCTTTACA GTGTTGAAAC CTTTGTGAA AAACCAGCTC CAGAGGACGC 420
 TCCTAGCGAC CTTGCTATTA TCGGACGCTA CCTCCTCACG CCTGAAATTT TTGAGATTCT 480
 CGAAAAGCAA GCTCCAGGTG CAGGAAATGA AATTCAGCTG ACAGATGCAA TCGACACCCT 540
 CAATAAACA CAACGTGTAT TTGCTCGTGA GTTCAAAGGG GCTCGTTACG ATGTCGGAGA 600
 CAAGTTTGGC TTCATGAAAA CATCCATCGA CTACGCCCTC AAACACCCAC AAGTCAAAGA 660
 TGATTTGAAG AATTACCTCA TCCAATTGG AAAAGAATTG ACTGAGAAGG AA 712

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Arg Ser Ile Glu Asp His Phe Asp Ser Asn Phe Glu Leu Glu Tyr Asn
 1 5 10 15
 Leu Lys Glu Lys Gly Lys Thr Asp Leu Leu Lys Leu Val Asp Lys Thr
 20 25 30
 Thr Asp Met Arg Leu His Phe Ile Arg Gln Thr His Pro Arg Gly Leu
 35 40 45
 Gly Asp Ala Val Leu Gln Ala Lys Ala Phe Val Gly Asn Glu Pro Phe
 50 55 60
 Val Val Met Leu Gly Asp Asp Leu Met Asp Ile Thr Asp Glu Lys Ala
 65 70 75 80
 Val Pro Leu Thr Lys Gln Leu Met Asp Asp Tyr Glu Arg Thr His Ala
 85 90 95
 Ser Thr Ile Ala Val Met Pro Val Pro His Asp Glu Val Ser Ala Tyr
 100 105 110
 Gly Val Ile Ala Pro Gln Gly Glu Gly Lys Asp Gly Leu Tyr Ser Val
 115 120 125
 Glu Thr Phe Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser Asp Leu
 130 135 140
 Ala Ile Ile Gly Arg Tyr Leu Leu Thr Pro Glu Ile Phe Glu Ile Leu
 145 150 155 160

Glu Lys Gln Ala Pro Gly Ala Gly Asn Glu Ile Gln Leu Thr Asp Ala
 165 170 175

Ile Asp Thr Leu Asn Lys Thr Gln Arg Val Phe Ala Arg Glu Phe Lys
 180 185 190

Gly Ala Arg Tyr Asp Val Gly Asp Lys Phe Gly Phe Met Lys Thr Ser
 195 200 205

Ile Asp Tyr Ala Leu Lys His Pro Gln Val Lys Asp Asp Leu Lys Asn
 210 215 220

Tyr Leu Ile Gln Leu Gly Lys Glu Leu Thr Glu Lys Glu
 225 230 235

(2) INFORMATION FOR SEQ ID NO: 137:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CGCTCAAAAT ACCAGAGGTG TTCAGCTAAT CGAGCACGTT TCTCCTCAAA TGTGAAAGC 60

CCAATTGGAG AGTGTCTTTT CTGATATTCC ACCTCAGGCT GTAAAACTG GAATGTTGGC 120

TACTACTGAA ATCATGGAAA TCATCCAACC CTATCTTAAA AAAGTGGATT GTCCCTATGT 180

CCTTGATCCT GTTATGGTTG CTACAAGTGG AGATGCCTTG ATTGACTCAA ATGCTAGAGA 240

CTATCTCAAA ACAAACTTAC TACCTCTAGC AACTATTATT ACGCCAAATC TTCCTGAAGC 300

AGAAGAGATT GTTGGTTTTT CAATCCATGA CCCCGAAGAC ATGCAGCGTG CTGGTCGCCT 360

GATTTTAAAA GAATTTGGTC CTCAGTCTGT GGTATCAAAA GCGGACATC TCAAAGGTGG 420

TGCTAAAGAT TTCCTCTTTA CCAAGAATGA ACAATTTGTC TGGGAAAGCC CACGAATTCA 480

AACCTGTCAC ACCCATGGTA CT 502

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 167 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Ala Gln Asn Thr Arg Gly Val Gln Leu Ile Glu His Val Ser Pro Gln
 1 5 10 15

Met Leu Lys Ala Gln Leu Glu Ser Val Phe Ser Asp Ile Pro Pro Gln
 20 25 30

Ala Val Lys Thr Gly Met Leu Ala Thr Thr Glu Ile Met Glu Ile Ile
 35 40 45

Gln Pro Tyr Leu Lys Lys Leu Asp Cys Pro Tyr Val Leu Asp Pro Val
 50 55 60

Met Val Ala Thr Ser Gly Asp Ala Leu Ile Asp Ser Asn Ala Arg Asp
 65 70 75 80

Tyr Leu Lys Thr Asn Leu Leu Pro Leu Ala Thr Ile Ile Thr Pro Asn
 85 90 95

Leu Pro Glu Ala Glu Glu Ile Val Gly Phe Ser Ile His Asp Pro Glu
 100 105 110

Asp Met Gln Arg Ala Gly Arg Leu Ile Leu Lys Glu Phe Gly Pro Gln
 115 120 125

Ser Val Val Ile Lys Gly Gly His Leu Lys Gly Gly Ala Lys Asp Phe
 130 135 140

Leu Phe Thr Lys Asn Glu Gln Phe Val Trp Glu Ser Pro Arg Ile Gln
 145 150 155 160

Thr Cys His Thr His Gly Thr
 165

a' ent.
 (2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 805 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

AATTGTACAA TTAGAAAAAG ATAGCAAATC AGACAAAGAA CAAGTTGATA AACTATTTGA	60
ATCATTGTGAT GCATCTTCAG ATGAATCTAT TTCTAAATTA AAAGAACTAT CTGAAACTTC	120
ACTTAAAACC GATGCAGGTA AAGACTATCT TAATAACAAA GTCAAAGAAT CATCTAAAGC	180
AATTGTAGAT TTTCATTTGC AAAAAGGTTT GGCTTATGAT GTTAAAGATT CAGATGACAA	240
ATTTAAAGAT AAAGCAACTC TTGAAACAAA TGTAAGAGAA ATTACAAAAC AAATTGATTT	300
TATCAAAAAA GTTGATGAAA CTTTAAACA AGAGAATTTG GAAGAACTC TTAAATCTCT	360
AAATGATCTT GTTGATAAAT ATCAAAAACA AATCGAACTT TTGAAGAAAG AAGAAGAAAA	420
AGCTGCTGAA AAAGCTGCTG AAAAAGCAAA GGAATCTTCT AGTCAAAGTA ATTCTTCTGG	480
TAGTGCTTCT AATGAGTCTT ATAATGGATC TTCCAATTCA AATGTAGATT ATAGTTCATC	540
TGAACAAACT AATGGATATT CAAATAATTA TGGCGGTCAA GATTATTCTG GTTCAGGAGA	600
TAGTTCAACA AATGGTGGAT CATCAGAACA ATATTCATCT AGCAATTCAA ACAGCGGAGC	660

AAATAATGTC TACAGATATA AAGGCACTGG TGCTGACGGC TATCAAAGAT ACTACTACAA 720
 AGATCATAAT AATGGAGATG TGTATGATGA CGATGGAAAT TACCTTGGGA ACTTTGGTGG 780
 CGGCATTGCA GAACCTAGTC AACGC 805

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Ile Val Gln Leu Glu Lys Asp Ser Lys Ser Asp Lys Glu Gln Val Asp
 1 5 10 15
 Lys Leu Phe Glu Ser Phe Asp Ala Ser Ser Asp Glu Ser Ile Ser Lys
 20 25 30
 Leu Lys Glu Leu Ser Glu Thr Ser Leu Lys Thr Asp Ala Gly Lys Asp
 35 40 45
 Tyr Leu Asn Asn Lys Val Lys Glu Ser Ser Lys Ala Ile Val Asp Phe
 50 55 60
 His Leu Gln Lys Gly Leu Ala Tyr Asp Val Lys Asp Ser Asp Asp Lys
 65 70 75 80
 Phe Lys Asp Lys Ala Thr Leu Glu Thr Asn Val Lys Glu Ile Thr Lys
 85 90 95
 Gln Ile Asp Phe Ile Lys Lys Val Asp Glu Thr Phe Lys Gln Glu Asn
 100 105 110
 Leu Glu Glu Thr Leu Lys Ser Leu Asn Asp Leu Val Asp Lys Tyr Gln
 115 120 125
 Lys Gln Ile Glu Leu Leu Lys Lys Glu Glu Glu Lys Ala Ala Glu Lys
 130 135 140
 Ala Ala Glu Lys Ala Lys Glu Ser Ser Ser Gln Ser Asn Ser Ser Gly
 145 150 155 160
 Ser Ala Ser Asn Glu Ser Tyr Asn Gly Ser Ser Asn Ser Asn Val Asp
 165 170 175
 Tyr Ser Ser Ser Glu Gln Thr Asn Gly Tyr Ser Asn Asn Tyr Gly Gly
 180 185 190
 Gln Asp Tyr Ser Gly Ser Gly Asp Ser Ser Thr Asn Gly Gly Ser Ser
 195 200 205
 Glu Gln Tyr Ser Ser Ser Asn Ser Asn Ser Gly Ala Asn Asn Val Tyr
 210 215 220

Arg Tyr Lys Gly Thr Gly Ala Asp Gly Tyr Gln Arg Tyr Tyr Tyr Lys
225 230 235 240

Asp His Asn Asn Gly Asp Val Tyr Asp Asp Asp Gly Asn Tyr Leu Gly
245 250 255

Asn Phe Gly Gly Gly Ile Ala Glu Pro Ser Gln Arg
260 265

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TCTGACCAAG CAAAAAGAAG CAGTCAATGA CAAAGGAAAA GCAGCTGTTG TTAAGGTGGT 60
GGAAAGCCAG GCAGAACTTT ATAGCTTAGA AAAGAATGAA GATGCTAGCC TAAGAAAGTT 120
ACAAGCAGAT GGACGCATCA CGGAAGAACA GGCTAAAGCT TATAAAGAAT ACAATGATAA 180
AAATGGAGGA GCAAATCGTA AAGTCAATGA T 211

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Leu Thr Lys Gln Lys Glu Ala Val Asn Asp Lys Gly Lys Ala Ala Val
1 5 10 15
Val Lys Val Val Glu Ser Gln Ala Glu Leu Tyr Ser Leu Glu Lys Asn
20 25 30
Glu Asp Ala Ser Leu Arg Lys Leu Gln Ala Asp Gly Arg Ile Thr Glu
35 40 45
Glu Gln Ala Lys Ala Tyr Lys Glu Tyr Asn Asp Lys Asn Gly Gly Ala
50 55 60
Asn Arg Lys Val Asn Asp
65 70

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

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GTCCGGCTCT GTCCAGTCCA CTTTTTCAGC GGTAGAGGAA CAGATTTTCT TTATGGAGTT      60
TGAAGAACTC TATCGGGAAA CCCAAAAACG CAGTGTAGCC AGTCAGCAA AGACTAGTCT      120
GAACCTAGAT GGGCAGACGC TTAGCAATGG CAGTCAAAAG TTGCCAGTCC CTAAAGGAAT      180
TCAGGCCCCA TCAGGCCAAA GTATTACATT TGACCGAGCT GGGGGCAATT CGTCCCTGGC      240
TAAGGTTGAA TTTTCAGACCA GTAAAGGAGC GATTGCTAT CAATTATATC TAGGAAATGG      300
AAAAATTAAA CGCATTAAGG AAACAAAAAA T                                     331

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(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

a' conf.

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Ser Gly Ser Val Gln Ser Thr Phe Ser Ala Val Glu Glu Gln Ile Phe
1           5           10           15
Phe Met Glu Phe Glu Glu Leu Tyr Arg Glu Thr Gln Lys Arg Ser Val
20          25          30
Ala Ser Gln Gln Lys Thr Ser Leu Asn Leu Asp Gly Gln Thr Leu Ser
35          40          45
Asn Gly Ser Gln Lys Leu Pro Val Pro Lys Gly Ile Gln Ala Pro Ser
50          55          60
Gly Gln Ser Ile Thr Phe Asp Arg Ala Gly Gly Asn Ser Ser Leu Ala
65          70          75          80
Lys Val Glu Phe Gln Thr Ser Lys Gly Ala Ile Arg Tyr Gln Leu Tyr
85          90          95
Leu Gly Asn Gly Lys Ile Lys Arg Ile Lys Glu Thr Lys Asn
100         105         110

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(2) INFORMATION FOR SEQ ID NO: 145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

GGGACAAATT CAAAAAATA GGCAAGAGGA AGCAAAATC TTGCAAAGG AAGAAGTCTT	60
GAGGGTAGCT AAGATGGCCC TGCAGACGGG GCAAAATCAG GTAAGCATCA ACGGAGTTGA	120
GATTCAGGTA TTTTCTAGTG AAAAAGGATT GGAGGTCTAC CATGGTTCAG AACAGTTGTT	180
GGCAATCAAA GAGCCA	196

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

a' Cont.

Gly	Gln	Ile	Gln	Lys	Asn	Arg	Gln	Glu	Glu	Ala	Lys	Ile	Leu	Gln	Lys	1	5	10	15
Glu	Glu	Val	Leu	Arg	Val	Ala	Lys	Met	Ala	Leu	Gln	Thr	Gly	Gln	Asn	20	25	30	
Gln	Val	Ser	Ile	Asn	Gly	Val	Glu	Ile	Gln	Val	Phe	Ser	Ser	Glu	Lys	35	40	45	
Gly	Leu	Glu	Val	Tyr	His	Gly	Ser	Glu	Gln	Leu	Leu	Ala	Ile	Lys	Glu	50	55	60	
Pro															65				

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

TCGCTACCAG CAACAAAGCG AGCAAAAGGA GTGGCTCTTG TTTGTGGACC AACTTGAGGT	60
AGAATTAGAC CGTTCGCAGT TCGAAAAGT AGAAGGCAAT CGCCTATACA TGAAGCAAGA	120
TGGCAAGGAC ATCGCCATCG GTAAGTCAAA GTCAGATGAT TTCCGTAAAA CGAATGCTCG	180
TGGTCGAGGT TATCAGCCTA TGGTTTATGG ACTCAAATCT GTACGGATTA CAGAGGACAA	240

TCAACTGGTT CGCTTTCATT TCCAGTTCCA AAAAGGCTTA GAAAGGGAGT TCATCTATCG 300
 TGTGGAAAAA GAAAAAAGT 319

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Arg Tyr Gln Gln Gln Ser Glu Gln Lys Glu Trp Leu Leu Phe Val Asp
 1 5 10 15
 Gln Leu Glu Val Glu Leu Asp Arg Ser Gln Phe Glu Lys Val Glu Gly
 20 25 30
 Asn Arg Leu Tyr Met Lys Gln Asp Gly Lys Asp Ile Ala Ile Gly Lys
 35 40 45
 Ser Lys Ser Asp Asp Phe Arg Lys Thr Asn Ala Arg Gly Arg Gly Tyr
 50 55 60
 Gln Pro Met Val Tyr Gly Leu Lys Ser Val Arg Ile Thr Glu Asp Asn
 65 70 75 80
 Gln Leu Val Arg Phe His Phe Gln Phe Gln Lys Gly Leu Glu Arg Glu
 85 90 95
 Phe Ile Tyr Arg Val Glu Lys Glu Lys Ser
 100 105

(2) INFORMATION FOR SEQ ID NO: 149:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

GAACCGACAA GTCGCCCACT ATCAAGACTA TGCTTTGAAT AAAGAAAAAT TGTTTGCTTT 60
 TGCTATGGCT AAACGAACCA AAGATAAGGT TGAGCAAGAA AGTGGGAAC ACTTTTTTAA 120
 TCTAGGTCAG GTAAGCTATC AAAACAAGAA AACTGGCTTA GTGACGAGGG TTCGTACGGA 180
 TAAGAGCCAA TATGAGTTTC TGTTTCCTTC AGTCAAAATC AAAGAAGAGA AAAGAGATAA 240
 AAAGGAAGAG GTAGCGACCG ATTCAAGCGA AAAAGTGGAG AAGAAAAAAT CAGAAGAGAA 300

GCCTGAAAAG AAAGAGAATT CA

322

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Asn Arg Gln Val Ala His Tyr Gln Asp Tyr Ala Leu Asn Lys Glu Lys
 1 5 10 15

Leu Val Ala Phe Ala Met Ala Lys Arg Thr Lys Asp Lys Val Glu Gln
 20 25 30

Glu Ser Gly Glu Gln Phe Phe Asn Leu Gly Gln Val Ser Tyr Gln Asn
 35 40 45

Lys Lys Thr Gly Leu Val Thr Arg Val Arg Thr Asp Lys Ser Gln Tyr
 50 55 60

Glu Phe Leu Phe Pro Ser Val Lys Ile Lys Glu Glu Lys Arg Asp Lys
 65 70 75 80

Lys Glu Glu Val Ala Thr Asp Ser Ser Glu Lys Val Glu Lys Lys Lys
 85 90 95

Ser Glu Glu Lys Pro Glu Lys Lys Glu Asn Ser
 100 105

(2) INFORMATION FOR SEQ ID NO: 151:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 784 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

GGTTGTCGGC TGGCAATATA TCCCGTTTCC ATCTAAAGGT AGTACAATTG GTCCTTACCC 60

AAATGGTATC AGATTAGAAG GTTTTCCAAA GTCAGAGTGG TACTACTTCG ATAAAAATGG 120

AGTGCTACAA GAGTTTGTGTG GTTGGAAC AACATTAGAGATT AAAACTAAAG ACAGTGTGG 180

AAGAAAGTAC GGGGAAAAAC GTGAAGATTC AGAAGATAAA GAAGAGAAGC GTTATTATAC 240

GAAGTATTAC TTTAATCAAA ATCATTCCTT AGAGACAGGT TGGCTTTATG ATCAGTCTAA 300

CTGGTATTAT CTAGCTAAGA CGGAAATTAA TGGAGAAAAC TACCTTGGTG GTGAAAGACG 360

TGCGGGGTGG ATAAACGATG ATTCGACTTG GTACTACCTA GATCCAACAA CTGGTATTAT 420

GCAAACAGGT TGGCAATATC TAGGTAATAA GTGGTACTAC CTCCGTTCTT CAGGAGCAAT 480
 GGCCACTGGC TGGTATCAGG AAGGTACCAC TTGGTATTAT TTAGACCACC CAAATGGCGA 540
 TATGAAAACA GGTGGCAAAA ACCTTGGGAA CAAATGGTAC TATCTCCGTT CATCAGGAGC 600
 TATGGCAACT GGTGGTATC AAGATGGTTC AACTTGGTAC TACCTAAATG CAGGTAATGG 660
 AGACATGAAG ACAGGTTGGT TCCAGGTCAA TGGCAACTGG TACTATGCTT ATAGCTCAGG 720
 TGCTTTGGCA GTGAATACGA CCGTAGATGG CTATTCTGTC AACTATAATG GCGAATGGGT 780
 TCGG 784

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Val Val Gly Trp Gln Tyr Ile Pro Phe Pro Ser Lys Gly Ser Thr Ile
 1 5 10 15
 Gly Pro Tyr Pro Asn Gly Ile Arg Leu Glu Gly Phe Pro Lys Ser Glu
 20 25 30
 Trp Tyr Tyr Phe Asp Lys Asn Gly Val Leu Gln Glu Phe Val Gly Trp
 35 40 45
 Lys Thr Leu Glu Ile Lys Thr Lys Asp Ser Val Gly Arg Lys Tyr Gly
 50 55 60
 Glu Lys Arg Glu Asp Ser Glu Asp Lys Glu Glu Lys Arg Tyr Tyr Thr
 65 70 75 80
 Asn Tyr Tyr Phe Asn Gln Asn His Ser Leu Glu Thr Gly Trp Leu Tyr
 85 90 95
 Asp Gln Ser Asn Trp Tyr Tyr Leu Ala Lys Thr Glu Ile Asn Gly Glu
 100 105 110
 Asn Tyr Leu Gly Gly Glu Arg Arg Ala Gly Trp Ile Asn Asp Asp Ser
 115 120 125
 Thr Trp Tyr Tyr Leu Asp Pro Thr Thr Gly Ile Met Gln Thr Gly Trp
 130 135 140
 Gln Tyr Leu Gly Asn Lys Trp Tyr Tyr Leu Arg Ser Ser Gly Ala Met
 145 150 155 160
 Ala Thr Gly Trp Tyr Gln Glu Gly Thr Thr Trp Tyr Tyr Leu Asp His
 165 170 175

Pro Asn Gly Asp Met Lys Thr Gly Trp Gln Asn Leu Gly Asn Lys Trp
 180 185 190

Tyr Tyr Leu Arg Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Asp
 195 200 205

Gly Ser Thr Trp Tyr Tyr Leu Asn Ala Gly Asn Gly Asp Met Lys Thr
 210 215 220

Gly Trp Phe Gln Val Asn Gly Asn Trp Tyr Tyr Ala Tyr Ser Ser Gly
 225 230 235 240

Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Ser Val Asn Tyr Asn
 245 250 255

Gly Glu Trp Val Arg
 260

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

a' cont.

GGCCAAATCA GAATGGGTAG AAGACAAGGG AGCCTTTTAT TATCTTGACC AAGATGGAAA	60
GATGAAAAGA AATGCTTGGG TAGGAACTTC CTATGTTGGT GCAACAGGTG CCAAAGTAAT	120
AGAAGACTGG GTCTATGATT CTCAATACGA TGCTTGGTTT TATATCAAAG CAGATGGACA	180
GCACGCAGAG AAAGAATGGC TCCAAATTAA AGGGAAGGAC TATTATTTCA AATCCGGTGG	240
TTATCTACTG ACAAGTCAGT GGATTAATCA AGCTTATGTG AATGCTAGTG GTGCCAAAGT	300
ACAGCAAGGT TGGCTTTTTG ACAAACAATA CCAATCTTGG TTTTACATCA AAGAAAATGG	360
AAACTATGCT GATAAAGAAT GGATTTTCGA GAATGGTCAC TATTATTATC TAAAATCCGG	420
TGGCTACATG GCAGCCAATG AATGGATTG GGATAAGGAA TCTTGGTTTT ATCTCAAATT	480
TGATGGGAAA ATGGCTGAAA AAGAATGGGT CTACGATTCT CATAGTCAAG CTGGTACTA	540
CTTCAAATCC GGTGGTTACA TGACAGCCAA TGAATGGATT TGGGATAAGG AATCTTGGTT	600
TTATCTCAAA TCTGATGGGA AAATAGCTGA AAAAGAATGG GTCTACGATT CTCATAGTCA	660
AGCTTGGTAC TACTTCAAAT CCGGTGGTTA CATGACAGCC AATGAATGGA TTTGGGATTA	720
GGAATCTTGG TTTTACCTCA AATCTGATGG GAAAATAGCT GAAAAAGAAT GGGTCTACGA	780
TTCTCATAGT CAAGCTTGGT ACTACTTCAA ATCTGGTGGC TACATGGCGA AAAATGAGAC	840
AGTAGATGGT TATCAGCTTG GAAGCGATGG TAAATGGCTT GGAGGAAAAA CTACAAATGA	900
AAATGCTGCT TACTATCAAG TAGTGCCTGT TACAGCCAAT GTTTATGATT CAGATGGTGA	960
AAAGCTTTCC TATATATCGC AAGGTAGTGT CGTATGGCTA GATAAGGATA GAAAAAGTGA	1020

264

TGACAAGCGC TTGGCTATTA CTATTTCTGG TTTGTCAGGC TATATGAAAA CAGAAGATTT 1080
 ACAAGCGCTA GATGCTAGTA AGGACTTTAT CCCTTATTAT GAGAGTGATG GCCACCGTTT 1140
 TTATCACTAT GTGGCTCAGA ATGCTAGTAT CCCAGTAGCT TCTCATCTTT CTGATATGGA 1200
 AGTAGGCAAG AAATATTATT CGGCAGATGG CCTGCATTTT GATGGTTTTA AGCTTGAGAA 1260
 TCCCTTCCTT TTCAAAGATT TAACAGAGGC TACAAACTAC AGTGCTGAAG AATTGGATAA 1320
 GGTATTTAGT TTGCTAAACA TTAACAATAG CCTTTTGGAG AACAAAGGCG CTACTTTTAA 1380
 GGAAGCCGAA GAACATTACC ATATCAATGC TCTTTATCTC CTTGCCCATTA GTGCCCTAGA 1440
 AAGTAAGTGG GGAAGAAGTA AAATTGCCAA AGATAAGAAT AATTTCTTTG GCATTACAGC 1500
 CTATGATACG ACCCCTTACC TTTCTGCTAA GACATTTGAT GATGTGGATA AGGGAATTTT 1560
 AGGTGCAACC AAGTGGATTA AGGAAAATTA TATCGATAGG GGAAGAACTT TCCTTGGAAG 1620
 CAAGGCTTCT GGTATGAATG TGAATATGC TTCAGACCCT TATTGGGGCG AAAAAATTGC 1680
 TAGTGTGATG ATGAAAATCA ATGAGAAG 1708

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 569 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Ala Lys Ser Glu Trp Val Glu Asp Lys Gly Ala Phe Tyr Tyr Leu Asp
 1 5 10 15
 Gln Asp Gly Lys Met Lys Arg Asn Ala Trp Val Gly Thr Ser Tyr Val
 20 25 30
 Gly Ala Thr Gly Ala Lys Val Ile Glu Asp Trp Val Tyr Asp Ser Gln
 35 40 45
 Tyr Asp Ala Trp Phe Tyr Ile Lys Ala Asp Gly Gln His Ala Glu Lys
 50 55 60
 Glu Trp Leu Gln Ile Lys Gly Lys Asp Tyr Tyr Phe Lys Ser Gly Gly
 65 70 75 80
 Tyr Leu Leu Thr Ser Gln Trp Ile Asn Gln Ala Tyr Val Asn Ala Ser
 85 90 95
 Gly Ala Lys Val Gln Gln Gly Trp Leu Phe Asp Lys Gln Tyr Gln Ser
 100 105 110
 Trp Phe Tyr Ile Lys Glu Asn Gly Asn Tyr Ala Asp Lys Glu Trp Ile
 115 120 125

Phe Glu Asn Gly His Tyr Tyr Tyr Leu Lys Ser Gly Gly Tyr Met Ala
 130 135 140
 Ala Asn Glu Trp Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Phe
 145 150 155 160
 Asp Gly Lys Met Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln
 165 170 175
 Ala Trp Tyr Tyr Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp
 180 185 190
 Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile
 195 200 205
 Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr
 210 215 220
 Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp Ile Trp Asp Lys
 225 230 235 240
 Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile Ala Glu Lys Glu
 245 250 255
 Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr Phe Lys Ser Gly
 260 265 270
 Gly Tyr Met Ala Lys Asn Glu Thr Val Asp Gly Tyr Gln Leu Gly Ser
 275 280 285
 Asp Gly Lys Trp Leu Gly Gly Lys Thr Thr Asn Glu Asn Ala Ala Tyr
 290 295 300
 Tyr Gln Val Val Pro Val Thr Ala Asn Val Tyr Asp Ser Asp Gly Glu
 305 310 315 320
 Lys Leu Ser Tyr Ile Ser Gln Gly Ser Val Val Trp Leu Asp Lys Asp
 325 330 335
 Arg Lys Ser Asp Asp Lys Arg Leu Ala Ile Thr Ile Ser Gly Leu Ser
 340 345 350
 Gly Tyr Met Lys Thr Glu Asp Leu Gln Ala Leu Asp Ala Ser Lys Asp
 355 360 365
 Phe Ile Pro Tyr Tyr Glu Ser Asp Gly His Arg Phe Tyr His Tyr Val
 370 375 380
 Ala Gln Asn Ala Ser Ile Pro Val Ala Ser His Leu Ser Asp Met Glu
 385 390 395 400
 Val Gly Lys Lys Tyr Tyr Ser Ala Asp Gly Leu His Phe Asp Gly Phe
 405 410 415
 Lys Leu Glu Asn Pro Phe Leu Phe Lys Asp Leu Thr Glu Ala Thr Asn
 420 425 430
 Tyr Ser Ala Glu Glu Leu Asp Lys Val Phe Ser Leu Leu Asn Ile Asn
 435 440 445
 Asn Ser Leu Leu Glu Asn Lys Gly Ala Thr Phe Lys Glu Ala Glu Glu
 450 455 460

His Tyr His Ile Asn Ala Leu Tyr Leu Leu Ala His Ser Ala Leu Glu
 465 470 475 480

Ser Asn Trp Gly Arg Ser Lys Ile Ala Lys Asp Lys Asn Asn Phe Phe
 485 490 495

Gly Ile Thr Ala Tyr Asp Thr Thr Pro Tyr Leu Ser Ala Lys Thr Phe
 500 505 510

Asp Asp Val Asp Lys Gly Ile Leu Gly Ala Thr Lys Trp Ile Lys Glu
 515 520 525

Asn Tyr Ile Asp Arg Gly Arg Thr Phe Leu Gly Asn Lys Ala Ser Gly
 530 535 540

Met Asn Val Glu Tyr Ala Ser Asp Pro Tyr Trp Gly Glu Lys Ile Ala
 545 550 555 560

Ser Val Met Met Lys Ile Asn Glu Lys
 565

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 946 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

ATTTCGAGAT GATTCTGAAG GATGGCAGTT TGTCCAAGAA AATGGTAGAA CCTACTACAA 60

AAAGGGGGAT CTAAAAGAAA CCTACTGGAG AGTGATAGAT GGGAAGTACT ATTATTTTGA 120

TCCTTTATCC GGAGAGATGG TTGTCGGCTG GCAATATATA CCTGCTCCAC ACAAGGGGGT 180

TACGATTGGT CCTTCTCCAA GAATAGAGAT TGCTCTTAGA CCAGATTGGT TTTATTTTGG 240

TCAAGATGGT GTATTACAAG AATTTGTTGG CAAGCAAGTT TTAGAAGCAA AACTGCTAC 300

GAATACCAAC AAACATCATG GGGAAGAATA TGATAGCCAA GCAGAGAAAC GACTCTATTA 360

TTTTGAAGAT CAGCGTAGTT ATCATACTTT AAAAAGTGGT TGGATTATATG AAGAGGGTCA 420

TTGGTATTAT TTACAGAAGG ATGGTGGCTT TGATTCGCGC ATCAACAGAT TGACGGTTGG 480

AGAGCTAGCA CGTGGTTGGG TTAAGGATTA CCCTCTTACG TATGATGAAG AGAAGCTAAA 540

AGCAGCTCCA TGGTACTATC TAAATCCAGC AACTGGCATT ATGCAAACAG GTTGGCAATA 600

TCTAGGTAAT AGATGGTACT ACCTCCATTC GTCAGGAGCT ATGGCAACTG GCTGGTATAA 660

GGAAGGCTCA ACTTGGTACT ATCTAGATGC TGAAAATGGT GATATGAGAA CTGGCTGGCA 720

AAACCTTGGG AACAAATGGT ACTATCTCCG TTCATCAGGA GCTATGGCAA CTGGTTGGTA 780

TCAGGAAAGT TCGACTTGGT ACTATCTAAA TGCAAGTAAT GGAGATATGA AAACAGGCTG 840

GTTCCAAGTC AATGGTAACT GGTACTATGC CTATGATTCA GGTGCTTTAG CTGTTAATAC 900

CACAGTAGGT GGTACTACT TAACTATAA TGGTGAATGG GTTAAG

946

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Val Phe Ala Asp Asp Ser Glu Gly Trp Gln Phe Val Gln Glu Asn Gly
 1 5 10 15
 Arg Thr Tyr Tyr Lys Lys Gly Asp Leu Lys Glu Thr Tyr Trp Arg Val
 20 25 30
 Ile Asp Gly Lys Tyr Tyr Tyr Phe Asp Pro Leu Ser Gly Glu Met Val
 35 40 45
 Val Gly Trp Gln Tyr Ile Pro Ala Pro His Lys Gly Val Thr Ile Gly
 50 55 60
 Pro Ser Pro Arg Ile Glu Ile Ala Leu Arg Pro Asp Trp Phe Tyr Phe
 65 70 75 80
 Gly Gln Asp Gly Val Leu Gln Glu Phe Val Gly Lys Gln Val Leu Glu
 85 90 95
 Ala Lys Thr Ala Thr Asn Thr Asn Lys His His Gly Glu Glu Tyr Asp
 100 105 110
 Ser Gln Ala Glu Lys Arg Val Tyr Tyr Phe Glu Asp Gln Arg Ser Tyr
 115 120 125
 His Thr Leu Lys Thr Gly Trp Ile Tyr Glu Glu Gly His Trp Tyr Tyr
 130 135 140
 Leu Gln Lys Asp Gly Gly Phe Asp Ser Arg Ile Asn Arg Leu Thr Val
 145 150 155 160
 Gly Glu Leu Ala Arg Gly Trp Val Lys Asp Tyr Pro Leu Thr Tyr Asp
 165 170 175
 Glu Glu Lys Leu Lys Ala Ala Pro Trp Tyr Tyr Leu Asn Pro Ala Thr
 180 185 190
 Gly Ile Met Gln Thr Gly Trp Gln Tyr Leu Gly Asn Arg Trp Tyr Tyr
 195 200 205
 Leu His Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Lys Glu Gly Ser
 210 215 220
 Thr Trp Tyr Tyr Leu Asp Ala Glu Asn Gly Asp Met Arg Thr Gly Trp
 225 230 235 240

Gln Asn Leu Gly Asn Lys Trp Tyr Tyr Leu Arg Ser Ser Gly Ala Met
245 250 255

Ala Thr Gly Trp Tyr Gln Glu Ser Ser Thr Trp Tyr Tyr Leu Asn Ala
260 265 270

Ser Asn Gly Asp Met Lys Thr Gly Trp Phe Gln Val Asn Gly Asn Trp
275 280 285

Tyr Tyr Ala Tyr Asp Ser Gly Ala Leu Ala Val Asn Thr Thr Val Gly
290 295 300

Gly Tyr Tyr Leu Asn Tyr Asn Gly Glu Trp Val Lys
305 310 315

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

TGTCGCTGCA AATGAACTG AAGTAGCAAA AACTTCGCAG GATACAACGA CAGCTTCAAG 60
 TAGTTTCAGAG CAAAATCAGT CTTCTAATAA AACGCAAACG AGCGCAGAAG TACAGACTAA 120
 TGCTGCTGCC CACTGGGATG GGGATTATTA TGTAAAGGAT GATGGTTCTA AAGCTCAAAG 180
 TGAATGGATT TTTGACAAC TACTATAAGGC TTGGTTTTAT ATTAATTCAG ATGGTCGTTA 240
 CTCGCAGAAT GAATGGCATG GAAATTACTA CCTGAAATCA GGTGGATATA TGGCCCCAAA 300
 CGAGTGGATC TATGACAGTA ATTACAAGAG TTGGTTTTAT CTCAAGTCAG ATGGGGCTTA 360
 TGCTCATCAA GAATGGCAAT TGATTGGAAA TAAGTGGTAC TACTTCAAGA AGTGGGGTTA 420
 CATGGCTAAA AGCCAATGGC AAGGAAGTTA TTTCTTGAAT GGTCAAGGAG CTATGATGCA 480
 AAATGAATGG CTCTATGAT CCAGCCTATT CTGCTTATTT TTATCTAAAA TCCGATGGAA 540
 CTTATGCTAA CCAAGAGTGG CAAAAGTGG GCGGCAAATG GTACTATTTT AAGAAGTGGG 600
 GCTATATGGC TCGGAATGAG TGGCAAGGCA ACTACTATTT GACTGGAAGT GGTGCCATGG 660
 CGACTGACGA AGTGATTATG GATGGTACTC GCTATATCTT TCGGCCTCT GGTGAGCTCA 720
 AAGAAAAAAA AGATTTGAAT GTCGGCTGGG TTCACAGAGA TGGTAAGCGC TATTTCTTTA 780
 ATAATAGAGA AGAACAAGTG GGAACCGAAC ATGCTAAGAA AGTCATTGAT ATTAGTGAGC 840
 ACAATGGTCG TATCAATGAT TGGAAAAAGG TTATTGATGA GAACGAAGTG GATGGTGTCA 900
 TTGTTCTGCT AGGTTATAGC GGTAAAGAAG ACAAGGAATT GCGCATAAC ATTAAGGAGT 960
 TAAACCGTCT GGGAATTCCT TATGGTGTCT ATCTCTATAC CTATGCTGAA AATGAGACCG 1020
 ATGCTGAGAG TGACGCTAAA CAGACCATTG AACTTATAAA GAAATACAAT ATGAACCTGT 1080

CTTACCCTAT CTATTATGAT GTTGAGAATT GGGAATATGT AAATAAGAGC AAGAGAGCTC 1140
 CAAGTGATAC AGGCACTTGG GTTAAAATCA TCAACAAGTA CATGGACACG ATGAAGCAGG 1200
 CGGGTTATCA AAATGTGTAT GTCTATAGCT ATCGTAGTTT ATTACAGACG CGTTTAAAAC 1260
 ACCCAGATAT TTTAAAACAT GTAAACTGGG TAGCGGCCTA TACGAATGCT TTAGAATGGG 1320
 AAAACCCTCA TTATTCAGGA AAAAAAGGTT GGCAATATAC CTCTTCTGAA TACATGAAAG 1380
 GAATCCAAGG GCGCGTAGAT GTCAGCGTTT GGTAT 1415

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Val Ala Ala Asn Glu Thr Glu Val Ala Lys Thr Ser Gln Asp Thr Thr
 1 5 10 15
 Thr Ala Ser Ser Ser Ser Glu Gln Asn Gln Ser Ser Asn Lys Thr Gln
 20 25 30
 Thr Ser Ala Glu Val Gln Thr Asn Ala Ala Ala His Trp Asp Gly Asp
 35 40 45
 Tyr Tyr Val Lys Asp Asp Gly Ser Lys Ala Gln Ser Glu Trp Ile Phe
 50 55 60
 Asp Asn Tyr Tyr Lys Ala Trp Phe Tyr Ile Asn Ser Asp Gly Arg Tyr
 65 70 75 80
 Ser Gln Asn Glu Trp His Gly Asn Tyr Tyr Leu Lys Ser Gly Gly Tyr
 85 90 95
 Met Ala Gln Asn Glu Trp Ile Tyr Asp Ser Asn Tyr Lys Ser Trp Phe
 100 105 110
 Tyr Leu Lys Ser Asp Gly Ala Tyr Ala His Gln Glu Trp Gln Leu Ile
 115 120 125
 Gly Asn Lys Trp Tyr Tyr Phe Lys Lys Trp Gly Tyr Met Ala Lys Ser
 130 135 140
 Gln Trp Gln Gly Ser Tyr Phe Leu Asn Gly Gln Gly Ala Met Met Gln
 145 150 155 160
 Asn Glu Trp Leu Tyr Asp Pro Ala Tyr Ser Ala Tyr Phe Tyr Leu Lys
 165 170 175
 Ser Asp Gly Thr Tyr Ala Asn Gln Glu Trp Gln Lys Val Gly Gly Lys
 180 185 190

a'
cont.

Trp Tyr Tyr Phe Lys Lys Trp Gly Tyr Met Ala Arg Asn Glu Trp Gln
 195 200 205
 Gly Asn Tyr Tyr Leu Thr Gly Ser Gly Ala Met Ala Thr Asp Glu Val
 210 215 220
 Ile Met Asp Gly Thr Arg Tyr Ile Phe Ala Ala Ser Gly Glu Leu Lys
 225 230 235 240
 Glu Lys Lys Asp Leu Asn Val Gly Trp Val His Arg Asp Gly Lys Arg
 245 250 255
 Tyr Phe Phe Asn Asn Arg Glu Glu Gln Val Gly Thr Glu His Ala Lys
 260 265 270
 Lys Val Ile Asp Ile Ser Glu His Asn Gly Arg Ile Asn Asp Trp Lys
 275 280 285
 Lys Val Ile Asp Glu Asn Glu Val Asp Gly Val Ile Val Arg Leu Gly
 290 295 300
 Tyr Ser Gly Lys Glu Asp Lys Glu Leu Ala His Asn Ile Lys Glu Leu
 305 310 315 320
 Asn Arg Leu Gly Ile Pro Tyr Gly Val Tyr Leu Tyr Thr Tyr Ala Glu
 325 330 335
 Asn Glu Thr Asp Ala Glu Ser Asp Ala Lys Gln Thr Ile Glu Leu Ile
 340 345 350
 Lys Lys Tyr Asn Met Asn Leu Ser Tyr Pro Ile Tyr Tyr Asp Val Glu
 355 360 365
 Asn Trp Glu Tyr Val Asn Lys Ser Lys Arg Ala Pro Ser Asp Thr Gly
 370 375 380
 Thr Trp Val Lys Ile Ile Asn Lys Tyr Met Asp Thr Met Lys Gln Ala
 385 390 395 400
 Gly Tyr Gln Asn Val Tyr Val Tyr Ser Tyr Arg Ser Leu Leu Gln Thr
 405 410 415
 Arg Leu Lys His Pro Asp Ile Leu Lys His Val Asn Trp Val Ala Ala
 420 425 430
 Tyr Thr Asn Ala Leu Glu Trp Glu Asn Pro His Tyr Ser Gly Lys Lys
 435 440 445
 Gly Trp Gln Tyr Thr Ser Ser Glu Tyr Met Lys Gly Ile Gln Gly Arg
 450 455 460
 Val Asp Val Ser Val Trp Tyr
 465 470

(2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1924 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

TACGTCTCAG CCTACTTTTG TAAGAGCAGA AGAATCTCCA CAAGTTGTCTG AAAAATCTTC 60
 ATTAGAGAAG AAATATGAGG AAGCAAAAGC AAAAGCTGAT ACTGCCAAGA AAGATTACGA 120
 AACGGCTAAA AAGAAAGCAG AAGACGCTCA GAAAAAGTAT GAAGATGATC AGAAGAGAAC 180
 TGAGGAGAAA GCTCGAAAAG AAGCAGAAGC ATCTCAAAAA TTGAATGATG TGGCGCTTGT 240
 TGTTCAAAAT GCATATAAAG AGTACCGAGA AGTTCAAAAT CAACGTAGTA AATATAAATC 300
 TGACGCTGAA TATCAGAAAA AATTAACAGA GGTGCTACTT AAAATAGAGA AGGCTAGGAA 360
 AGAGCAACAG GACTTGCAAA ATAAATTTAA TGAAGTAAGA GCAGTTGTAG TTCCTGAACC 420
 AAATGCGTTG GCTGAGACTA AGAAAAAGC AGAAGAAGCT AAAGCAGAAG AAAAAGTAGC 480
 TAAGAGAAAA TATGATTATG CAACTCTAAA GGTAGCACTA CGAAGAAAAG AAGTAGAGGC 540
 TAAGGAACCT GAAATTGAAA AACTTCAATA TGAAATTTCT ACTTTGGAAC AAGAAGTTGC 600
 TACTGCTCAA CATCAAGTAG ATAATTTGAA AAAACTTCTT GCTGGTGCGG ATCCTGATGA 660
 TGGCACAGAA GTTATAGAAG CTAAATTTAA AAAAGGAGAA GCTGAGCTAA ACGCTAAACA 720
 AGCTGAGTTA GCAAAAAAAC AAACAGAACT TGAAAACTT CTTGACAGCC TTGATCCTGA 780
 AGGTAAGACT CAGGATGAAT TAGATAAAGA AGCAGAAGAA GCTGAGTTGG ATAAAAAGC 840
 TGATGAACTT CAAAATAAAG TTGCTGATTT AGAAAAAGAA ATTAGTAACC TTGAAATAIT 900
 ACTTGGAGGG GCTGATNCTG AAGATGATAC TGCTGCTCTT CAAAATAAAT TAGCTACTAA 960
 AAAAGCTGAA TTGGAAAAAA CTCAAAAAGA ATTAGATGCA GCTCTTAATG AGTTAGGCC 1020
 TGATGGAGAT GAAGAAGAAA CTCCAGCGCC GGCTCCTCAA CCAGAGCAAC CAGCTCCTGC 1080
 ACCAAAACCA GAGCAACCAG CTCCAGCTCC AAAACCAGAG CAACCAGCTC CTGCACCAAA 1140
 ACCAGAGCAA CCAGCTCCAG CTCCAAAACC AGAGCAACCA GCTCCAGCTC CAAAACCAGA 1200
 GCAACCAGCT AAGCCGGAGA AACCAGCTGA AGAGCCTACT CAACCAGAAA AACCAGCCAC 1260
 TCCAAAAACA GGCTGGAAAC AAGAAAACGG TATGTGGTAT TTCTACAATA CTGATGGTTC 1320
 AATGGCAATA GGTGGGCTCC AAAACAACGG TTCATGGTAC TACCTAAACG CTAACGGCGC 1380
 TATGGCAACA GGTGGGTGA AAGATGGAGA TACCTGGTAC TATCTTGAAG CATCAGGTGC 1440
 TATGAAAGCA AGCCAATGGT TCAAAGTATC AGATAAATGG TACTATGTCA ACAGCAATGG 1500
 CGCTATGGCG ACAGGCTGGC TCCAATACAA TGGCTCATGG TACTACCTCA ACGCTAATGG 1560
 TGATATGGCG ACAGGATGGC TCCAATACAA CGGTTTCATGG TATTACCTCA ACGCTAATGG 1620
 TGATATGGCG ACAGGATGGG CTAAAGTCAA CGGTTTCATGG TACTACCTAA ACGCTAACGG 1680
 TGCTATGGCT ACAGGTTGGG CTAAAGTCAA CGGTTTCATGG TACTACCTAA ACGCTAACGG 1740
 TTCAATGGCA ACAGGTTGGG TGAAAGATGG AGATACCTGG TACTATCTTG AAGCATCAGG 1800

TGCTATGAAA GCAAGCCAAT GGTTCAAAGT ATCAGATAAA TGGTACTATG TCAATGGCTT 1860
 AGGTGCCCTT GCAGTCAACA CAACTGTAGA TGGCTATAAA GTCAATGCCA ATGGTGAATG 1920
 GGTT 1924

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 641 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Thr Ser Gln Pro Thr Phe Val Arg Ala Glu Glu Ser Pro Gln Val Val
 1 5 10 15
 Glu Lys Ser Ser Leu Glu Lys Lys Tyr Glu Glu Ala Lys Ala Lys Ala
 20 25 30
 Asp Thr Ala Lys Lys Asp Tyr Glu Thr Ala Lys Lys Lys Ala Glu Asp
 35 40 45
 Ala Gln Lys Lys Tyr Glu Asp Asp Gln Lys Arg Thr Glu Glu Lys Ala
 50 55 60
 Arg Lys Glu Ala Glu Ala Ser Gln Lys Leu Asn Asp Val Ala Leu Val
 65 70 75 80
 Val Gln Asn Ala Tyr Lys Glu Tyr Arg Glu Val Gln Asn Gln Arg Ser
 85 90 95
 Lys Tyr Lys Ser Asp Ala Glu Tyr Gln Lys Lys Leu Thr Glu Val Asp
 100 105 110
 Ser Lys Ile Glu Lys Ala Arg Lys Glu Gln Gln Asp Leu Gln Asn Lys
 115 120 125
 Phe Asn Glu Val Arg Ala Val Val Val Pro Glu Pro Asn Ala Leu Ala
 130 135 140
 Glu Thr Lys Lys Lys Ala Glu Glu Ala Lys Ala Glu Glu Lys Val Ala
 145 150 155 160
 Lys Arg Lys Tyr Asp Tyr Ala Thr Leu Lys Val Ala Leu Ala Lys Lys
 165 170 175
 Glu Val Glu Ala Lys Glu Leu Glu Ile Glu Lys Leu Gln Tyr Glu Ile
 180 185 190
 Ser Thr Leu Glu Gln Glu Val Ala Thr Ala Gln His Gln Val Asp Asn
 195 200 205
 Leu Lys Lys Leu Leu Ala Gly Ala Asp Pro Asp Asp Gly Thr Glu Val
 210 215 220

Ile Glu Ala Lys Leu Lys Lys Gly Glu Ala Glu Leu Asn Ala Lys Gln
 225 230 235 240
 Ala Glu Leu Ala Lys Lys Gln Thr Glu Leu Glu Lys Leu Leu Asp Ser
 245 250 255
 Leu Asp Pro Glu Gly Lys Thr Gln Asp Glu Leu Asp Lys Glu Ala Glu
 260 265 270
 Glu Ala Glu Leu Asp Lys Lys Ala Asp Glu Leu Gln Asn Lys Val Ala
 275 280 285
 Asp Leu Glu Lys Glu Ile Ser Asn Leu Glu Ile Leu Leu Gly Gly Ala
 290 295 300
 Asp Xaa Glu Asp Asp Thr Ala Ala Leu Gln Asn Lys Leu Ala Thr Lys
 305 310 315 320
 Lys Ala Glu Leu Glu Lys Thr Gln Lys Glu Leu Asp Ala Ala Leu Asn
 325 330 335
 Glu Leu Gly Pro Asp Gly Asp Glu Glu Glu Thr Pro Ala Pro Ala Pro
 340 345 350
 Gln Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Pro
 355 360 365
 Ala Pro Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro
 370 375 380
 Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu
 385 390 395 400
 Gln Pro Ala Lys Pro Glu Lys Pro Ala Glu Glu Pro Thr Gln Pro Glu
 405 410 415
 Lys Pro Ala Thr Pro Lys Thr Gly Trp Lys Gln Glu Asn Gly Met Trp
 420 425 430
 Tyr Phe Tyr Asn Thr Asp Gly Ser Met Ala Ile Gly Trp Leu Gln Asn
 435 440 445
 Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly
 450 455 460
 Trp Val Lys Asp Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala
 465 470 475 480
 Met Lys Ala Ser Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val
 485 490 495
 Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser
 500 505 510
 Trp Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr Gly Trp Leu Gln
 515 520 525
 Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr
 530 535 540
 Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly
 545 550 555 560

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TGGACAGGTG	AAAGGTCATG	CTACATTGT	GAAATCCATG	ACAACTGAAA	TGTACCAAGA	60
ACAACAGAAC	CATTCTCTCG	CCTACAATCA	ACGCTTGGNT	TCGCAAAATC	GCATTGTAGA	120
TCCTTTTTTTG	GCGGAGGGAT	ATGAGGTCAA	TTACCAAGTG	TCTGACGACC	CTGATGCAGT	180
CTATGGTTAC	TTGTCTATTC	CAAGTTTGGA	AATCATGGAG	CCGGTTTATT	TGGGAGCAGA	240
TTATCATCAT	TTAGGGATGG	GCTTGGCTCA	TGTGGATGGT	ACACCGCTGC	CTCTGGATGG	300
TACAGGGATT	CGCTCAGTGA	TTGCTGGGCA	CCGTGCAGAG	CCAAGCCATG	TCTTTTTCCG	360
CCATTTGGAT	CAGCTAAAAG	TTGGAGATGC	TCTTTATTAT	GATAATGGCC	AGGAAATTGT	420
AGAATATCAG	ATGATGGACA	CAGAGATTAT	TTTACCGTCG	GAATGGGAAA	AATTAGAATC	480
GGTAGCTCT	AAAAATATCA	TGACCTTGAT	AACCTGCGAT	CCGATTCCTA	CCTTTAATAA	540
ACGCTTATTA	GTGAATTTTG	AACGAGTCGC	TGTTTATCAA	AAATCAGATC	CACAAACAGC	600
TGCAGTTGCG	AGGGTTGCTT	TTACGAAAGA	AGGACAATCT	GTATCGCGTG	TTGCAACCTC	660
TCAATGGTTG						670

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Gly Gln Val Lys Gly His Ala Thr Phe Val Lys Ser Met Thr Thr Glu
 1 5 10 15
 Met Tyr Gln Glu Gln Gln Asn His Ser Leu Ala Tyr Asn Gln Arg Leu
 20 25 30
 Xaa Ser Gln Asn Arg Ile Val Asp Pro Phe Leu Ala Glu Gly Tyr Glu
 35 40 45
 Val Asn Tyr Gln Val Ser Asp Asp Pro Asp Ala Val Tyr Gly Tyr Leu
 50 55 60
 Ser Ile Pro Ser Leu Glu Ile Met Glu Pro Val Tyr Leu Gly Ala Asp
 65 70 75 80
 Tyr His His Leu Gly Met Gly Leu Ala His Val Asp Gly Thr Pro Leu
 85 90 95
 Pro Leu Asp Gly Thr Gly Ile Arg Ser Val Ile Ala Gly His Arg Ala
 100 105 110
 Glu Pro Ser His Val Phe Phe Arg His Leu Asp Gln Leu Lys Val Gly
 115 120 125
 Asp Ala Leu Tyr Tyr Asp Asn Gly Gln Glu Ile Val Glu Tyr Gln Met
 130 135 140
 Met Asp Thr Glu Ile Ile Leu Pro Ser Glu Trp Glu Lys Leu Glu Ser
 145 150 155 160
 Val Ser Ser Lys Asn Ile Met Thr Leu Ile Thr Cys Asp Pro Ile Pro
 165 170 175
 Thr Phe Asn Lys Arg Leu Leu Val Asn Phe Glu Arg Val Ala Val Tyr
 180 185 190
 Gln Lys Ser Asp Pro Gln Thr Ala Ala Val Ala Arg Val Ala Phe Thr
 195 200 205
 Lys Glu Gly Gln Ser Val Ser Arg Val Ala Thr Ser Gln Trp Leu
 210 215 220

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

GATTGCTCCT TTGAAGGATT TGAGAGAAAC CATGTTGGAA ATTGCTTCTG GTGCTCAAAA 60
 TCTTCGTGCC AAGGAAGTTG GTGCCTATGA ACTGAGAGAA GTAAC TCGCC AATTTAATGC 120

TATGTTGGAT CAGATTGATC AGTTGATGGT AGCTATTTCGT AGCCAGGAAG AAACGACCCG 180
TCAGTACCAA CTTCAAGCCC TTTCGAGCCA GATTAATCCA CATTTCTCTCT ATAACACTTT 240
GGACACCATC ATCTGGATGG CTGAATTTCA TGATAGTCAG CGAGTGGTGC AGGTGACCAA 300
GTCCTTGGCA ACCTATTTCC GCTTGGCGCT CAATCAAGGC AAGGACTTGA TTTGTCTCTC 360
TGACGAAATC AATCATGTCC GCCAGTATCT CTTTATCCAG AAACAACGCT ATGGAGATAA 420
GCTGGAATAC GAAATTAATG AAAATGTTGC CTTTGATAAT TTAGTCTTAC CCAAGCTGGT 480
CCTACAACCC CTTGTAGAAA ATGCTCTTTA CCATGGCATT AAGGAAAAGG AAGGTCAGGG 540
CCATATTAAA CTTTCTGTCC AGAAACAGGA TTCGGGATTG GTCATCCGTA TTGAGGATGA 600
TGGCGTTGGC TTCCAAGATG CTGGTGATAG TAGTCAAAGT CAACTCAAAC GTGGGGGAGT 660
TGGTCTTCAA AATGTCGATC AACGGCTCAA ACTTCATTTT GGAGCCAATT ACCATATGAA 720
GATTGATTCT AGACCCCAAA AAGGGACGAA AGTTGAAATA TATATAAATA GAATAGAAAC 780
TAGC 784

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ile Ala Pro Leu Lys Asp Leu Arg Glu Thr Met Leu Glu Ile Ala Ser
1 5 10 15
Gly Ala Gln Asn Leu Arg Ala Lys Glu Val Gly Ala Tyr Glu Leu Arg
20 25 30
Glu Val Thr Arg Gln Phe Asn Ala Met Leu Asp Gln Ile Asp Gln Leu
35 40 45
Met Val Ala Ile Arg Ser Gln Glu Glu Thr Thr Arg Gln Tyr Gln Leu
50 55 60
Gln Ala Leu Ser Ser Gln Ile Asn Pro His Phe Leu Tyr Asn Thr Leu
65 70 75 80
Asp Thr Ile Ile Trp Met Ala Glu Phe His Asp Ser Gln Arg Val Val
85 90 95
Gln Val Thr Lys Ser Leu Ala Thr Tyr Phe Arg Leu Ala Leu Asn Gln
100 105 110
Gly Lys Asp Leu Ile Cys Leu Ser Asp Glu Ile Asn His Val Arg Gln
115 120 125

Tyr Leu Phe Ile Gln Lys Gln Arg Tyr Gly Asp Lys Leu Glu Tyr Glu
 130 135 140
 Ile Asn Glu Asn Val Ala Phe Asp Asn Leu Val Leu Pro Lys Leu Val
 145 150 155 160
 Leu Gln Pro Leu Val Glu Asn Ala Leu Tyr His Gly Ile Lys Glu Lys
 165 170 175
 Glu Gly Gln Gly His Ile Lys Leu Ser Val Gln Lys Gln Asp Ser Gly
 180 185 190
 Leu Val Ile Arg Ile Glu Asp Asp Gly Val Gly Phe Gln Asp Ala Gly
 195 200 205
 Asp Ser Ser Gln Ser Gln Leu Lys Arg Gly Gly Val Gly Leu Gln Asn
 210 215 220
 Val Asp Gln Arg Leu Lys Leu His Phe Gly Ala Asn Tyr His Met Lys
 225 230 235 240
 Ile Asp Ser Arg Pro Gln Lys Gly Thr Lys Val Glu Ile Tyr Ile Asn
 245 250 255
 Arg Ile Glu Thr Ser
 260

(2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

TAGGTCATAT GGGACTTTTT TTCTACAACA AAATAGGCTC CATAATATCT ATAAGGGATT 60
 TACCCACTAC AAATATTATA GAGCCGAAAA TTCACATCTA ATATATGCAG ACTACTTTGA 120
 AATGAAATTA AAAAAATTAT TAAAGGATGA CACAAAAGTT TTTGAAAAAT CTACATTCAA 180
 ATTTGTAGAA GGATATAAAA TATACCTGAC AGAATCTAAA GAATCTGGAA TTAAACAAAT 240
 GGACAATGTC ATAAAAATAT TTGAGTTTAT TGAATCTAAA AGTATTGCTT TATATTTTCA 300
 AAAACGATTA AATGAGCTGA TAGAT 325

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Arg	Ser	Tyr	Gly	Thr	Phe	Phe	Leu	Gln	Gln	Asn	Arg	Leu	His	Asn	Ile
1				5					10					15	
Tyr	Lys	Gly	Phe	Thr	His	Tyr	Lys	Tyr	Tyr	Arg	Ala	Glu	Asn	Ser	His
			20					25					30		
Leu	Ile	Tyr	Ala	Asp	Tyr	Phe	Glu	Met	Lys	Leu	Lys	Lys	Leu	Leu	Lys
		35					40					45			
Asp	Asp	Thr	Lys	Val	Phe	Glu	Lys	Ser	Thr	Phe	Lys	Phe	Val	Glu	Gly
	50					55					60				
Tyr	Lys	Ile	Tyr	Leu	Thr	Glu	Ser	Lys	Glu	Ser	Gly	Ile	Lys	Gln	Met
65					70					75					80
Asp	Asn	Val	Ile	Lys	Tyr	Phe	Glu	Phe	Ile	Glu	Ser	Lys	Ser	Ile	Ala
			85						90					95	
Leu	Tyr	Phe	Gln	Lys	Arg	Leu	Asn	Glu	Leu	Ile	Asp				
			100					105							

(2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

CAACGTTGAG AATTATTTGC GAATGTGTTT GGATAGCATT CAGAATCAGA CGTATCAAAA	60
TTTGTAGTGT TTATTAATCA ATGATGGCTC TCCAGATCAT TCATCCAAAA TATGTGAAGA	120
ATTTGTAGAG AAAGATTCTC GTTTCAAATA TTTTGAGAAA GCAAACGGCG GTCTTTTCATC	180
AGCTCGTAAC CTAGGTATTG AATGTTCCGGG GGGGGGCGTA CATTACTTTT GTAGACTC	238

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Asn	Val	Glu	Asn	Tyr	Leu	Arg	Met	Cys	Leu	Asp	Ser	Ile	Gln	Asn	Gln
1				5					10					15	

Thr Tyr Gln Asn Phe Glu Cys Leu Leu Ile Asn Asp Gly Ser Pro Asp
 20 25 30

His Ser Ser Lys Ile Cys Glu Glu Phe Val Glu Lys Asp Ser Arg Phe
 35 40 45

Lys Tyr Phe Glu Lys Ala Asn Gly Gly Leu Ser Ser Ala Arg Asn Leu
 50 55 60

Gly Ile Glu Cys Ser Gly Gly Gly Val His Tyr Phe Cys Arg Leu
 65 70 75

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

CTACTATCAA TCAAGTTCTT CAGCCATTGA GGCCACCATT GAGGGCAACA GCCAAACGAC 60

CATCAGCCAG ACTAGCCACT TTATTGAGTC TTATATCAAA AACTAGAAA CCACCTCGAC 120

TGGTTTGACC CAGCAGACGG ATGTTCTGGC CTATGCTGAG AATCCCAGTC AAGACAAGGT 180

CGAGGGAATC CGAGATTGTG TTTTGACCAT CTTGAAGTCA GATAAGGACT TGAAAAGTGT 240

TGTGCTGGTG ACCAAATCTG GTCAGGTCAT TTCTACAGAT GACAGTGTGC AGATGAAAAC 300

TTCTCTGAT ATGATGGCTG AGGATTGGTA CCAAAGGCC ATTCATCAGG GAGCTATGCC 360

TGTTTTGACT CCAGCTCGTA AATCAGATAG TCAGTGGGTC ATTTCTGTCA CTCAAGAACT 420

TGTTGATGCA AAGGGAGCCA ATCTTGGTGT GCTTCGTTTG GATATTCTTT ATGAAACTCT 480

GGAAGCCTAT CTCAATCAAC TCCAGTTGGG GCAGCAGGGC TTTGCCTTCA TTATCAATGA 540

AAACCATGAA TTTGTCTACC ATCCTCAACA CACAGTTTAT AGTTCGTCTA GCAAAATGGA 600

GGCTATGAAA CCCTACATCG ATACAGGTCA GGGTTATACT CCTGGTCACA AATCCTACGT 660

CAGTCAAGAG AAGATTGCAG GAACTGATTG GACGGTGCTT GCGTGTCAT CATTGGAAAA 720

GTTAGACCAG GTTCGGAGTC AG 742

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Tyr Tyr Gln Ser Ser Ser Ser Ala Ile Glu Ala Thr Ile Glu Gly Asn
 1 5 10 15
 Ser Gln Thr Thr Ile Ser Gln Thr Ser His Phe Ile Gln Ser Tyr Ile
 20 25 30
 Lys Lys Leu Glu Thr Thr Ser Thr Gly Leu Thr Gln Gln Thr Asp Val
 35 40 45
 Leu Ala Tyr Ala Glu Asn Pro Ser Gln Asp Lys Val Glu Gly Ile Arg
 50 55 60
 Asp Leu Phe Leu Thr Ile Leu Lys Ser Asp Lys Asp Leu Lys Thr Val
 65 70 75 80
 Val Leu Val Thr Lys Ser Gly Gln Val Ile Ser Thr Asp Asp Ser Val
 85 90 95
 Gln Met Lys Thr Ser Ser Asp Met Met Ala Glu Asp Trp Tyr Gln Lys
 100 105 110
 Ala Ile His Gln Gly Ala Met Pro Val Leu Thr Pro Ala Arg Lys Ser
 115 120 125
 Asp Ser Gln Trp Val Ile Ser Val Thr Gln Glu Leu Val Asp Ala Lys
 130 135 140
 Gly Ala Asn Leu Gly Val Leu Arg Leu Asp Ile Ser Tyr Glu Thr Leu
 145 150 155 160
 Glu Ala Tyr Leu Asn Gln Leu Gln Leu Gly Gln Gln Gly Phe Ala Phe
 165 170 175
 Ile Ile Asn Glu Asn His Glu Phe Val Tyr His Pro Gln His Thr Val
 180 185 190
 Tyr Ser Ser Ser Ser Lys Met Glu Ala Met Lys Pro Tyr Ile Asp Thr
 195 200 205
 Gly Gln Gly Tyr Thr Pro Gly His Lys Ser Tyr Val Ser Gln Glu Lys
 210 215 220
 Ile Ala Gly Thr Asp Trp Thr Val Leu Gly Val Ser Ser Leu Glu Lys
 225 230 235 240
 Leu Asp Gln Val Arg Ser Gln
 245

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

GACAAAAACA TTAAACGTC CTGAGGTTTT ATCACCTGCA GGGACTTTAG AGAAGCTAAA

60

GGTAGCTGTT CAGTATGGAG CAGATGCTGT CTTTATCGGT GGTGAGGCCT ATGGTCTTCG 120
TAGCCGTGCG GGAAACTTTA CTTTCGAACA GATGGAAGAA GCGTGCAGT TTGCGGCCAA 180
GTATGGTGCC AAGGTCTATG TAGCGGCTAA TATGGTTATG CACGAAGGAA ATGAAGCTGG 240
TGCTGGTGAG TGGTTCGTA AACTGCGTGA TATCGGGATT GCAGCAGTTA TCGTATCTGA 300
CCCAGCCTTG ATTATGATTG CAGTGACTGA AGCACCAGGC CTTGAAATCC ACCTTTCTAC 360
CCAAGCCAGT GCCACTAACT ATGAAACCCCT TGAGTTCTGG AAAGAGCTAG GCTTGACTCG 420
TGTCGTTTAA GCGCGTGAGG TTTCAATGGA AGAATTAGCT GAGATCCGCA AACGTACAGA 480
TGTTGAAATT GAAGCCTTTG TCCATGGAGC TATGTGTATT TCATACTCTG GACGTTGTAC 540
TCTTTCAAAC CACATGAGTA TCGTGATGC CAACCGTGGT GGATGTTCTC AGTCATGCCG 600
TTGGAAATAC GACCTTTACG ATATGCCATT TGGGAAAGAA CGTAAGAGTT TGCAGGGTGA 660
GATTCCAGAA GAATTTTCAA TGTCAGCCGT TGACATGTCT ATGATTGACC ANATTCCAGA 720
TATGATTGAA AATGGTGTGG ACAGTCTAAA AATCGAAGGA CGTATGNAGT CTATTCACTA 780
NGTATCAACA GTAACCAACT GCTACAAGGC GGCTGTGGAT GCCTATCTTG AAAGTCCTGA 840
AAAGTTTGAA GCTATCAAAC AAGACTTGGT GGACGAGATG TGGAAGGTTG CCCAACGTGA 900
ACTGGCTACA GGATTTTACT ATGGTACACC ATCTGAAAAT GAGCAGTTGT TTGGTGCTCG 960
TCGTAAAATC CCTGAGTACA AGTTTGTGCG TGAAGTGGTT TCTTATGATG ATGCGGCACA 1020
AACAGCAACT ATTCGTCAAC GAAACGTCAT TAACGAAGGG GACCAAGTTG AGTTTATGG 1080
TCCAGGTTTC CGTCATTTTG AAACCTATAT TGAAGATTTG CATGATGCTA AAGGCAATAA 1140
AATCGACCGC GCTCCAAATC CAATGGAAC ATTGACTATT AAAGTCCCAC AACCTGTTCA 1200
ATCAGGAGAC ATGGTTCGAG CTCTTAAAGA GGGGCTTATC AATCTTTATA AGGAAGATGG 1260
AACCAGCGTC ACAGTTCGTG CT 1282

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 427 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Thr Lys Thr Leu Lys Arg Pro Glu Val Leu Ser Pro Ala Gly Thr Leu
1 5 10 15
Glu Lys Leu Lys Val Ala Val Gln Tyr Gly Ala Asp Ala Val Phe Ile
20 25 30

Gly Gly Gln Ala Tyr Gly Leu Arg Ser Arg Ala Gly Asn Phe Thr Phe
 35 40 45
 Glu Gln Met Glu Glu Gly Val Gln Phe Ala Ala Lys Tyr Gly Ala Lys
 50 55 60
 Val Tyr Val Ala Ala Asn Met Val Met His Glu Gly Asn Glu Ala Gly
 65 70 75 80
 Ala Gly Glu Trp Phe Arg Lys Leu Arg Asp Ile Gly Ile Ala Ala Val
 85 90 95
 Ile Val Ser Asp Pro Ala Leu Ile Met Ile Ala Val Thr Glu Ala Pro
 100 105 110
 Gly Leu Glu Ile His Leu Ser Thr Gln Ala Ser Ala Thr Asn Tyr Glu
 115 120 125
 Thr Leu Glu Phe Trp Lys Glu Leu Gly Leu Thr Arg Val Val Leu Ala
 130 135 140
 Arg Glu Val Ser Met Glu Glu Leu Ala Glu Ile Arg Lys Arg Thr Asp
 145 150 155 160
 Val Glu Ile Glu Ala Phe Val His Gly Ala Met Cys Ile Ser Tyr Ser
 165 170 175
 Gly Arg Cys Thr Leu Ser Asn His Met Ser Met Arg Asp Ala Asn Arg
 180 185 190
 Gly Gly Cys Ser Gln Ser Cys Arg Trp Lys Tyr Asp Leu Tyr Asp Met
 195 200 205
 Pro Phe Gly Lys Glu Arg Lys Ser Leu Gln Gly Glu Ile Pro Glu Glu
 210 215 220
 Phe Ser Met Ser Ala Val Asp Met Ser Met Ile Asp Xaa Ile Pro Asp
 225 230 235 240
 Met Ile Glu Asn Gly Val Asp Ser Leu Lys Ile Glu Gly Arg Met Xaa
 245 250 255
 Ser Ile His Xaa Val Ser Thr Val Thr Asn Cys Tyr Lys Ala Ala Val
 260 265 270
 Asp Ala Tyr Leu Glu Ser Pro Glu Lys Phe Glu Ala Ile Lys Gln Asp
 275 280 285
 Leu Val Asp Glu Met Trp Lys Val Ala Gln Arg Glu Leu Ala Thr Gly
 290 295 300
 Phe Tyr Tyr Gly Thr Pro Ser Glu Asn Glu Gln Leu Phe Gly Ala Arg
 305 310 315 320
 Arg Lys Ile Pro Glu Tyr Lys Phe Val Ala Glu Val Val Ser Tyr Asp
 325 330 335
 Asp Ala Ala Gln Thr Ala Thr Ile Arg Gln Arg Asn Val Ile Asn Glu
 340 345 350
 Gly Asp Gln Val Glu Phe Tyr Gly Pro Gly Phe Arg His Phe Glu Thr
 355 360 365

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Tyr Ile Glu Asp Leu His Asp Ala Lys Gly Asn Lys Ile Asp Arg Ala
 370 375 380

Pro Asn Pro Met Glu Leu Leu Thr Ile Lys Val Pro Gln Pro Val Gln
 385 390 395 400

Ser Gly Asp Met Val Arg Ala Leu Lys Glu Gly Leu Ile Asn Leu Tyr
 405 410 415

Lys Glu Asp Gly Thr Ser Val Thr Val Arg Ala
 420 425

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

TTCTCAGGAG ACCTTTAAAA ATATCACCAA TAGCTTCTCC ATGCAAATCA ATCGTCGCGT 60
 CAACCAAGGA ACGCCTCGTG GTGCTGGGAA TATCAAGGGT GAAGACATCA, AAAAAATCAC 120
 CGAAAACAAG GCCATTGAGT CTTATGTCAA ACGTATCAAC GCTATCGGAG ATTTGACTGG 180
 ATATGACCTG ATTGAAACGC CAGAAACCAA GAAGAATCTC ACTGCTGATC GTGCCAAGCG 240
 TTTTGGAAGT AGCTTGATGA TTACAGGTGT CAATGACTCC TCTAAAGAAG ACAAGTTTGT 300
 CTCTGGTTCT TATAAACTAG TCGAAGGAGA GCACTTAACC AACGACGACA AGGATAAAAT 360
 CCTCTTGCAC AAGGACTTGG CAGCCAAACA CGGCTGGAAA GTAGGGGACA AGGTTAAACT 420
 GGACTCTAAT ATCTACGATG CAGATAATGA AAAAGGAGCC AAGGAAACAG TTGAAGTGAC 480
 AATCAAGGGA CTCTTTGATG GTCATAATAA GTCAGCAGTA ACCTACTCAC AAGAACTTTA 540
 CGAAAACACA GCTATTACAG ACATTACACAC TGCTGCAAAA CTTTATGGAT ACACAGAAGA 600
 CACAGCCATT TATGGGGACG CAACCTTCTT TGTAACAGCA GACAAGAACT TGGATGATGT 660
 TATGAAAGAG TTGAATGGCA TCAGTGGTAT CAACTGGAAG AGCTACACAC TCGTCAAGAG 720
 CTCCTCTAAC TACCCAGCTC TTGAGCAATC TATCTCTGGT ATGTACAAGA TGGCCAAC 778

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ser Gln Glu Thr Phe Lys Asn Ile Thr Asn Ser Phe Ser Met Gln Ile
 1 5 10 15
 Asn Arg Arg Val Asn Gln Gly Thr Pro Arg Gly Ala Gly Asn Ile Lys
 20 25 30
 Gly Glu Asp Ile Lys Lys Ile Thr Glu Asn Lys Ala Ile Glu Ser Tyr
 35 40 45
 Val Lys Arg Ile Asn Ala Ile Gly Asp Leu Thr Gly Tyr Asp Leu Ile
 50 55 60
 Glu Thr Pro Glu Thr Lys Lys Asn Leu Thr Ala Asp Arg Ala Lys Arg
 65 70 75 80
 Phe Gly Ser Ser Leu Met Ile Thr Gly Val Asn Asp Ser Ser Lys Glu
 85 90 95
 Asp Lys Phe Val Ser Gly Ser Tyr Lys Leu Val Glu Gly Glu His Leu
 100 105 110
 Thr Asn Asp Asp Lys Asp Lys Ile Leu Leu His Lys Asp Leu Ala Ala
 115 120 125
 Lys His Gly Trp Lys Val Gly Asp Lys Val Lys Leu Asp Ser Asn Ile
 130 135 140
 Tyr Asp Ala Asp Asn Glu Lys Gly Ala Lys Glu Thr Val Glu Val Thr
 145 150 155 160
 Ile Lys Gly Leu Phe Asp Gly His Asn Lys Ser Ala Val Thr Tyr Ser
 165 170 175
 Gln Glu Leu Tyr Glu Asn Thr Ala Ile Thr Asp Ile His Thr Ala Ala
 180 185 190
 Lys Leu Tyr Gly Tyr Thr Glu Asp Thr Ala Ile Tyr Gly Asp Ala Thr
 195 200 205
 Phe Phe Val Thr Ala Asp Lys Asn Leu Asp Asp Val Met Lys Glu Leu
 210 215 220
 Asn Gly Ile Ser Gly Ile Asn Trp Lys Ser Tyr Thr Leu Val Lys Ser
 225 230 235 240
 Ser Ser Asn Tyr Pro Ala Leu Glu Gln Ser Ile Ser Gly Met Tyr Lys
 245 250 255
 Met Ala Asn

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

AGTAAATGCG CAATCAAATT CATTAATATT AATAGATGAA CCTGAAATCT CACTTCATCC 60
 GAGTGCAATC TATAAAATTTA AAGAGTTTTT ACTTCAAGAG TGTTTAAATA AAAACATCA 120
 AATTATTATC ACTACACATT CTACACAACT TATAAAAGAT TTTCTAGAG AAGCCGTGAA 180
 ACTTTTAGTG AAAACGGAG AAAAGGTAGA TGTATTGAA AATATTGATT ATCAGGATGC 240
 ATTTTTTGAA TTAGGTGATG TGTATCATTC TAGGAAGATG ATTTATGTTG AAGATAGACT 300
 AGCTAAATAT ATTCTAGAGT TTGTTATCAC TCATTCAGGT AGTGAGAATC TTAAACAGAA 360
 TTTAGTAGTG AGATATATTC CTGGTGGAGC AAATCAAATA ATTTGTAATA ATATTTTAA 420
 CTCATCGTAT TTAGATTCCG ATAACCATTA TTTTGGCTT GATGGAGATC AAAACACTAA 480
 TGTTAGTGAA TCAAATAATT TAATGAACTA TCTTGAAAAT GGTGTTGTTA TATCAGATAA 540
 AATTCCTGAA TCAGATAATA AAAATCTTGA TGATATTATA AAATTGATAA NGGGATGTCC 600
 AATTAAATTT AATGTTTCAG GTAATAAAGG GCAAAAAAAT AATATTGAAT TAATTGCGAA 660
 ACAAAGAAGC TTTATAGATT ATTGGGCTAA ATAC 694

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Val Asn Ala Gln Ser Asn Ser Leu Ile Leu Ile Asp Glu Pro Glu Ile
 1 5 10 15
 Ser Leu His Pro Ser Ala Ile Tyr Lys Phe Lys Glu Phe Leu Leu Gln
 20 25 30
 Glu Cys Leu Asn Lys Lys His Gln Ile Ile Ile Thr Thr His Ser Thr
 35 40 45
 Gln Leu Ile Lys Asp Phe Pro Arg Glu Ala Val Lys Leu Leu Val Lys
 50 55 60
 Asn Gly Glu Lys Val Asp Val Ile Glu Asn Ile Asp Tyr Gln Asp Ala
 65 70 75 80
 Phe Phe Glu Leu Gly Asp Val Tyr His Ser Arg Lys Met Ile Tyr Val
 85 90 95
 Glu Asp Arg Leu Ala Lys Tyr Ile Leu Glu Phe Val Ile Thr His Ser
 100 105 110

Gly Ser Glu Asn Leu Lys Gln Asn Leu Val Val Arg Tyr Ile Pro Gly
 115 120 125

Gly Ala Asn Gln Ile Ile Cys Asn Asn Ile Leu Asn Ser Ser Tyr Leu
 130 135 140

Asp Ser Asp Asn His Tyr Phe Trp Leu Asp Gly Asp Gln Asn Thr Asn
 145 150 155 160

Val Ser Glu Ser Asn Asn Leu Met Asn Tyr Leu Glu Asn Gly Val Val
 165 170 175

Ile Ser Asp Lys Ile Pro Glu Ser Asp Asn Lys Asn Leu Asp Asp Ile
 180 185 190

Ile Lys Leu Ile Xaa Gly Cys Pro Ile Lys Phe Asn Val Ser Gly Asn
 195 200 205

Lys Gly Gln Lys Asn Asn Ile Glu Leu Ile Ala Lys Gln Arg Ser Phe
 210 215 220

Ile Asp Tyr Trp Ala Lys Tyr
 225 230

(2) INFORMATION FOR SEQ ID NO: 177:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 550 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

TTACCGCGTT CATCAAGATG TCAAACAAGT CATGACCTAT CAACCCATGG TCGGAGAAAT 60

ATTGAGTGAA CAAGACACCC CAGCAAACGA AGAGCTTG TG CTTGCTATGA TTTATACTGA 120

AACAAAAGGA AAAGAAGGCG ATGTTATGCA GTCTAGTGAG TCTGCAAGTG GTTCCACCAA 180

CACCATCAAT GATAATGCCT CTAGCATTCG GCAAGGCATT CAAACTCTGA CAGGCAATCT 240

CTATCTGGCG CAGAAGAAGG GGGTAGATAT CTGGACAGCT GTTCAAGCCT ATAATTTTGG 300

ACCTGCCTAT ATCGATTTTA TCGCCCAAAA TGGCAAGGAA AATACCCTGG CTCTAGCCAA 360

ACAGTACTCT CGTGAGACTG TTGCCCCCTT GCTTGGTAAT AGGACTGGAA AGACTTATAG 420

TTATATTCAC CCCATTTCCA TTTTTCACGG TGCTGAAC TC TATGTAAATG GAGGAACTA 480

TTATTATTCT AGACAGGTAC GACTTAACCT TTACATCATC AAATGTTTCA CTCTCTTTTC 540

AACATCTGGC 550

(2) INFORMATION FOR SEQ ID NO: 178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 183 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Tyr Arg Val His Gln Asp Val Lys Gln Val Met Thr Tyr Gln Pro Met
1 5 10 15

Val Arg Glu Ile Leu Ser Glu Gln Asp Thr Pro Ala Asn Glu Leu
20 25 30

Val Leu Ala Met Ile Tyr Thr Glu Thr Lys Gly Lys Glu Gly Asp Val
35 40 45

Met Gln Ser Ser Glu Ser Ala Ser Gly Ser Thr Asn Thr Ile Asn Asp
50 55 60

Asn Ala Ser Ser Ile Arg Gln Gly Ile Gln Thr Leu Thr Gly Asn Leu
65 70 75 80

Tyr Leu Ala Gln Lys Lys Gly Val Asp Ile Trp Thr Ala Val Gln Ala
85 90 95

Tyr Asn Phe Gly Pro Ala Tyr Ile Asp Phe Ile Ala Gln Asn Gly Lys
100 105 110

Glu Asn Thr Leu Ala Leu Ala Lys Gln Tyr Ser Arg Glu Thr Val Ala
115 120 125

Pro Leu Leu Gly Asn Arg Thr Gly Lys Thr Tyr Ser Tyr Ile His Pro
130 135 140

Ile Ser Ile Phe His Gly Ala Glu Leu Tyr Val Asn Gly Gly Asn Tyr
145 150 155 160

Tyr Tyr Ser Arg Gln Val Arg Leu Asn Leu Tyr Ile Ile Lys Cys Phe
165 170 175

Thr Leu Phe Ser Thr Ser Gly
180

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GTGGATGGGC TTAACTATC TTCGTATTCG CCGTGGCGCT AAAATTGTGG ACAATGAGGA 60

GTTTGAAGCC TTGATTCGTA CGGGTCAATT GATTGATTTG CGCGACCCAG CAGAATTCCA 120

CAGAAAACAT ATCCTTGGTG CACGCAATAT TCCTTCAAGT CAGTTGAAAA CTAGTCTTGC 180

AGCCCTTCGT AAAGATAAAC CTGTCCTTCT CTACGAAAAC CAACGTGCGC AACGAGTTAC 240

AAATGCAGCT CTTTACTTGA AAAACAAGG TTTTCTGAG ATTTATATCC TTTCTTATGG 300
 CTTGGATTCT TGGAAAGGA AAGTGAAGAC TAGC 334

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Trp Met Gly Phe Asn Tyr Leu Arg Ile Arg Arg Ala Ala Lys Ile Val
 1 5 10 15
 Asp Asn Glu Glu Phe Glu Ala Leu Ile Arg Thr Gly Gln Leu Ile Asp
 20 25 30
 Leu Arg Asp Pro Ala Glu Phe His Arg Lys His Ile Leu Gly Ala Arg
 35 40 45
 Asn Ile Pro Ser Ser Gln Leu Lys Thr Ser Leu Ala Ala Leu Arg Lys
 50 55 60
 Asp Lys Pro Val Leu Leu Tyr Glu Asn Gln Arg Ala Gln Arg Val Thr
 65 70 75 80
 Asn Ala Ala Leu Tyr Leu Lys Lys Gln Gly Phe Ser Glu Ile Tyr Ile
 85 90 95
 Leu Ser Tyr Gly Leu Asp Ser Trp Lys Gly Lys Val Lys Thr Ser
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 181:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

ACTAAACCAG CATCGTTCGC AGGAAAATAA GGACAATAAT CGTGTCTCTT ATGTGGATGG 60
 CAGCCAGTCA AGTCAGAAAA GTGAAAACCTT GACACCAGAC CAGGTTAGCC AGAAAGAAGG 120
 AATTCAGGCT GAGCAAATTG TAATCAAAAT TACAGATCAG GGCTATGTAA CGTCACACGG 180
 TGACCACTAT CATTACTATA ATGGGAAAGT TCCTTATGAT GCCCTCTTTA GTGAAGAACT 240
 CTTGATGAAG GATCCAAACT ATCAACTTAA AGACGCTGAT ATTGTCAATG AAGTCAAGGG 300

TGGTTATATC ATCAAGGTCG ATGGAAAATA TTATGTCTAC CTGAAAGATG CAGCTCATGC 360
 TGATAATGTT CGAACTAAAG ATGAAATCAA TCGTCAAAAA CAAGAACATG TCAAAGATAA 420
 TGAGAAGGTT AACTCTAATG TTGCTGTAGC AAGGTCTCAG GGACGATATA CGACAAATGA 480
 TGGTTATGTC TTTAATCCAG CTGATATTAT CGAAGATACG GGTAATGCTT ATATCGTTCC 540
 TCATGGAGGT CACTATCACT ACATTCCCAA AAGCGATTTA TCTGCTAGTG AATTAGCAGC 600
 AGCTAAAGCA CATCTGGCTG GAAAAATAT GCAACCGAGT CAGTTAAGCT ATTCTTCAAC 660
 AGCTAGTGAC AATAACACGC AATCTGTAGC AAAAGGATCA ACTAGCAAGC CAGCAAATAA 720
 ATCTGAAAAT CTCCAGAGTC TTTTGAAGGA ACTCTATGAT TCACCTAGCG CCCAACGTTA 780
 CAGTGAATCA GATGGCCTGG TCTTTGACCC TGCTAAGATT ATCAGTCGTA CACCAAATGG 840
 AGTTGCGATT CCGCATGGCG ACCATTACCA CTTTATTCTT TACAGCAAGC TTTCTGCCTT 900
 AGAAGAAAAG ATTGCCAGAA TGGTGCCTAT CAGTGGAAGT GGTTCCTACAG TTTCTACAAA 960
 TGCAAAACCT AATGAAGTAG TGTCTAGTCT AGGCAGTCTT TCAAGCAATC CTTCTTCTTT 1020
 AACGACAAGT AAGGAGCTCT CTTCAGCATC TGATGGTTAT ATTTTAAATC CAAAAGATAT 1080
 CGTGAAGAA ACGGCTACAG CTATATATGT AAGACATGGT GATCATTTCC ATTACATTCC 1140
 AAAATCAAAT CAAATTGGGC AACCGACTCT TCCAAACAAT AGTCTAGCAA CACCTTCTCC 1200
 ATCTCTTCCA ATCAATCCAG GAACTTCACA TGAGAAACAT GAAGAAGATG GATACGGATT 1260
 TGATGCTAAT CGTATTATCG CTGAAGATGA ATCAGGTTTT GTCATGAGTC ACGGAGACCA 1320
 CAATCATTAT TTCTTCAAGA AG 1342

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 447 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Leu	Asn	Gln	His	Arg	Ser	Gln	Glu	Asn	Lys	Asp	Asn	Asn	Arg	Val	Ser
1				5					10					15	
Tyr	Val	Asp	Gly	Ser	Gln	Ser	Ser	Gln	Lys	Ser	Glu	Asn	Leu	Thr	Pro
		20						25					30		
Asp	Gln	Val	Ser	Gln	Lys	Glu	Gly	Ile	Gln	Ala	Glu	Gln	Ile	Val	Ile
		35					40					45			
Lys	Ile	Thr	Asp	Gln	Gly	Tyr	Val	Thr	Ser	His	Gly	Asp	His	Tyr	His
	50					55						60			

Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe Ser Glu Glu Leu
 65 70 75 80
 Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala Asp Ile Val Asn
 85 90 95
 Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly Lys Tyr Tyr Val
 100 105 110
 Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg Thr Lys Asp Glu
 115 120 125
 Ile Asn Arg Gln Lys Gln Glu His Val Lys Asp Asn Glu Lys Val Asn
 130 135 140
 Ser Asn Val Ala Val Ala Arg Ser Gln Gly Arg Tyr Thr Thr Asn Asp
 145 150 155 160
 Gly Tyr Val Phe Asn Pro Ala Asp Ile Ile Glu Asp Thr Gly Asn Ala
 165 170 175
 Tyr Ile Val Pro His Gly Gly His Tyr His Tyr Ile Pro Lys Ser Asp
 180 185 190
 Leu Ser Ala Ser Glu Leu Ala Ala Ala Lys Ala His Leu Ala Gly Lys
 195 200 205
 Asn Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr Ala Ser Asp Asn
 210 215 220
 Asn Thr Gln Ser Val Ala Lys Gly Ser Thr Ser Lys Pro Ala Asn Lys
 225 230 235 240
 Ser Glu Asn Leu Gln Ser Leu Leu Lys Glu Leu Tyr Asp Ser Pro Ser
 245 250 255
 Ala Gln Arg Tyr Ser Glu Ser Asp Gly Leu Val Phe Asp Pro Ala Lys
 260 265 270
 Ile Ile Ser Arg Thr Pro Asn Gly Val Ala Ile Pro His Gly Asp His
 275 280 285
 Tyr His Phe Ile Pro Tyr Ser Lys Leu Ser Ala Leu Glu Glu Lys Ile
 290 295 300
 Ala Arg Met Val Pro Ile Ser Gly Thr Gly Ser Thr Val Ser Thr Asn
 305 310 315 320
 Ala Lys Pro Asn Glu Val Val Ser Ser Leu Gly Ser Leu Ser Ser Asn
 325 330 335
 Pro Ser Ser Leu Thr Thr Ser Lys Glu Leu Ser Ser Ala Ser Asp Gly
 340 345 350
 Tyr Ile Phe Asn Pro Lys Asp Ile Val Glu Glu Thr Ala Thr Ala Tyr
 355 360 365
 Ile Val Arg His Gly Asp His Phe His Tyr Ile Pro Lys Ser Asn Gln
 370 375 380
 Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro Ser Pro
 385 390 395 400

Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu Glu Asp
 405 410 415

Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu Ser Gly
 420 425 430

Phe Val Met Ser His Gly Asp His Asn His Tyr Phe Phe Lys Lys
 435 440 445

(2) INFORMATION FOR SEQ ID NO: 183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 934 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

TGACTACCTT GAAATCCCAC TTACAGCTA TCTGGTGA TTCAACTA AAGTTCTTCC 60
 AACTCCAATG ATGAACATCA TCAACGGTGG TTCTACTCT GACGCTCAA TCGCTTTCCA 120
 AGAGTTCATG ATCTTGCCAG TTGGTGCGCC AACATTTAAA GAAGCCCTTC GTTACGGTGC 180
 TGAAATCTTC CACGCTCTTA AGAAAATCCT TAAATCACGT GGTTTGGAAA CTGCCGTAGG 240
 TGACGAAGGT GGATTCGCTC CTCGTTTCGA AGGAACTGAA GATGGTGTG AACTATCCT 300
 TGCTGCGATT GAAGCTGCTG GATATGTACC AGGTAAAGAC GTATTTATCG GATTTGACTG 360
 TGCTTCATCA GAATTCTACG ATAAAGAACG TAAAGTTTAC GACTACACTA AATTTGAAGG 420
 TGAAGGTGCT GCTGTTGTA CATCTGCAGA ACAAATCGAC TACCTGAAG AATTGGTTAA 480
 CAAATACCCA ATCATCACTA TTGAAGATGG TATGGATGAA AACGACTGGG ATGGTTGGAA 540
 AGCTCTTACT GAACGTCTTG GTAAGAAAGT ACAACTTGTT GGTGACGACT TCTTCGTAAC 600
 AAACACTGAC TACCTTGCAC GTGGTATCCA AGAAGGTGCT GCTAACTCAA TCCTTATCAA 660
 AGTTAACCAA ATCGGTACTC TTAAGTAAAC TTTTGAAGCT ATCGAAATGG CTAAAGAAGC 720
 TGGTTACACT GCTGTTGTAT CACACCGTTC AGGTGAAACT GAAGATTCAA CAATCGCTGA 780
 TATTGCAGTT GCAACTAACG CAGGACAAAT CAAGACTGGT TCACTTTCAC GTACAGACCG 840
 CATCGCTAAA TACAACCAAT TGCTTCGTAT CGAAGACCAA CTTGGTGAAG TAGCTGAATA 900
 TCGTGGATG AAATCATTCT ACAACCTTAA AAAA 934

(2) INFORMATION FOR SEQ ID NO: 184:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 311 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Asp Tyr Leu Glu Ile Pro Leu Tyr Ser Tyr Leu Gly Gly Phe Asn Thr
 1 5 10 15
 Lys Val Leu Pro Thr Pro Met Met Asn Ile Ile Asn Gly Gly Ser His
 20 25 30
 Ser Asp Ala Pro Ile Ala Phe Gln Glu Phe Met Ile Leu Pro Val Gly
 35 40 45
 Ala Pro Thr Phe Lys Glu Ala Leu Arg Tyr Gly Ala Glu Ile Phe His
 50 55 60
 Ala Leu Lys Lys Ile Leu Lys Ser Arg Gly Leu Glu Thr Ala Val Gly
 65 70 75 80
 Asp Glu Gly Gly Phe Ala Pro Arg Phe Glu Gly Thr Glu Asp Gly Val
 85 90 95
 Glu Thr Ile Leu Ala Ala Ile Glu Ala Ala Gly Tyr Val Pro Gly Lys
 100 105 110
 Asp Val Phe Ile Gly Phe Asp Cys Ala Ser Ser Glu Phe Tyr Asp Lys
 115 120 125
 Glu Arg Lys Val Tyr Asp Tyr Thr Lys Phe Glu Gly Glu Gly Ala Ala
 130 135 140
 Val Arg Thr Ser Ala Glu Gln Ile Asp Tyr Leu Glu Glu Leu Val Asn
 145 150 155 160
 Lys Tyr Pro Ile Ile Thr Ile Glu Asp Gly Met Asp Glu Asn Asp Trp
 165 170 175
 Asp Gly Trp Lys Ala Leu Thr Glu Arg Leu Gly Lys Lys Val Gln Leu
 180 185 190
 Val Gly Asp Asp Phe Phe Val Thr Asn Thr Asp Tyr Leu Ala Arg Gly
 195 200 205
 Ile Gln Glu Gly Ala Ala Asn Ser Ile Leu Ile Lys Val Asn Gln Ile
 210 215 220
 Gly Thr Leu Thr Glu Thr Phe Glu Ala Ile Glu Met Ala Lys Glu Ala
 225 230 235 240
 Gly Tyr Thr Ala Val Val Ser His Arg Ser Gly Glu Thr Glu Asp Ser
 245 250 255
 Thr Ile Ala Asp Ile Ala Val Ala Thr Asn Ala Gly Gln Ile Lys Thr
 260 265 270
 Gly Ser Leu Ser Arg Thr Asp Arg Ile Ala Lys Tyr Asn Gln Leu Leu
 275 280 285
 Arg Ile Glu Asp Gln Leu Gly Glu Val Ala Glu Tyr Arg Gly Leu Lys
 290 295 300
 Ser Phe Tyr Asn Leu Lys Lys

305

310

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

TCGTATCTTT TTTTGGAGCA ATGTTTCGCGT AGAAGGACAT TCCATGGATC CGACCCTAGC 60
 GGATGGCGAA ATTCTCTTCG TTGTAAACA CCTTCCTATT GACCGTTTGT ATATCGTGGT 120
 GGCCCATGAG GAAGATGGCA ATAAGGACAT CGTCAAGCGC GTGATTGGAA TGCCTGGCGA 180
 CACCATTCTG TACGAAAATG ATAACTCTA CATCAATGAC AAAGAAACGG ACGAGCCTTA 240
 TCTAGCAGAC TATATCAAAC GCTTCAAGGA TGACAACTC CAAAGCACTT ACTCAGGCAA 300
 GGGCTTTGAA GGAAATAAAG GAACTTTCTT TAGAAGTATC GCTCAAAAAG CTCAAGCCTT 360
 CACAGTTGAT GTCAACTACA ACACCAACTT TAGCTTTACT GTTCCAGAAG GAGAATACCT 420
 TCTCTCGGA GATGACCGCT TGGTTTCGAG CGACAGCCGC CACGTAGGTA CCTTCAAAGC 480
 AAAAGATATC ACAGGGGAAG CTAAATCCG CTTATGGCCA ATCACCCGTA TCGGAACATT 540
 T 541

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Arg Ile Phe Phe Trp Ser Asn Val Arg Val Glu Gly His Ser Met Asp
 1 5 10 15
 Pro Thr Leu Ala Asp Gly Glu Ile Leu Phe Val Val Lys His Leu Pro
 20 25 30
 Ile Asp Arg Phe Asp Ile Val Val Ala His Glu Glu Asp Gly Asn Lys
 35 40 45
 Asp Ile Val Lys Arg Val Ile Gly Met Pro Gly Asp Thr Ile Arg Tyr
 50 55 60
 Glu Asn Asp Lys Leu Tyr Ile Asn Asp Lys Glu Thr Asp Glu Pro Tyr
 65 70 75 80

Leu Ala Asp Tyr Ile Lys Arg Phe Lys Asp Asp Lys Leu Gln Ser Thr
 85 90 95
 Tyr Ser Gly Lys Gly Phe Glu Gly Asn Lys Gly Thr Phe Phe Arg Ser
 100 105 110
 Ile Ala Gln Lys Ala Gln Ala Phe Thr Val Asp Val Asn Tyr Asn Thr
 115 120 125
 Asn Phe Ser Phe Thr Val Pro Glu Gly Glu Tyr Leu Leu Leu Gly Asp
 130 135 140
 Asp Arg Leu Val Ser Ser Asp Ser Arg His Val Gly Thr Phe Lys Ala
 145 150 155 160
 Lys Asp Ile Thr Gly Glu Ala Lys Phe Arg Leu Trp Pro Ile Thr Arg
 165 170 175
 Ile Gly Thr Phe
 180

(2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

GGACTCTCTC AAAGATGTGA AAGCAAATGC TAGCGACAGC AAGCCTGCAC AGGACAAGAA 60
 GGATGCAAAA CAAGGAACGG AAGATAGTAA GGATTCAGAT AAGATGACTG AAACAAACTC 120
 AGTTCCGGCA GGAGTGATTG TGGTCAGTCT ACTTGCCCTC CTAGGCGTGA TTGCCTTCTG 180
 GCTGATTTCGCG CGTAAGAAAG AGTCAGAAAT CCAGCAATTA AGCACGGAAT TGATCAAGGT 240
 TCTAGGACAG CTAGATGCAG AAAAAGCGGA TAAAAAAGTC CTTGCCAAAG CCCAAAACCT 300
 TCTCCAAGAA ACCCTTGATT TCGTGAAAGA AGAAAATGGC TCAGCAGAGA CAGAAACTAA 360
 ACTAGTAGAG GAGCTTAAAG CAATCCTTGA CAAACTCAAG 400

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Asp Ser Leu Lys Asp Val Lys Ala Asn Ala Ser Asp Ser Lys Pro Ala
 1 5 10 15
 Gln Asp Lys Lys Asp Ala Lys Gln Gly Thr Glu Asp Ser Lys Asp Ser
 20 25 30
 Asp Lys Met Thr Glu Thr Asn Ser Val Pro Ala Gly Val Ile Val Val
 35 40 45
 Ser Leu Leu Ala Leu Leu Gly Val Ile Ala Phe Trp Leu Ile Arg Arg
 50 55 60
 Lys Lys Glu Ser Glu Ile Gln Gln Leu Ser Thr Glu Leu Ile Lys Val
 65 70 75 80
 Leu Gly Gln Leu Asp Ala Glu Lys Ala Asp Lys Lys Val Leu Ala Lys
 85 90 95
 Ala Gln Asn Leu Leu Gln Glu Thr Leu Asp Phe Val Lys Glu Glu Asn
 100 105 110
 Gly Ser Ala Glu Thr Glu Thr Lys Leu Val Glu Glu Leu Lys Ala Ile
 115 120 125
 Leu Asp Lys Leu Lys
 130

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

CAAGAAATCC TATCATCTCT TCCAGAAGCA AACAGAGACG AGGGGAATTC AGACTCAGTT 60
 GATTGAAGAA TCGCTTAGTC AGCAGACTAT AATCCAGTCC TTCAATGCTC AAACAGAATT 120
 TATCCAAAGA TTGCGTGAGG CTCATGACAA CTACTCAGGC TATTCTCAGT CAGCCATCTT 180
 TTATTCTTCA ACGGTCAATC CTTGACTCG CTTTGTAAT GCACTCATTT ATGCCCTTTT 240
 AGCTGGAGTA GGAGCTTATC GTATCATGAT GGGTTCAGCC TTGACCGTCG GTCGTTTAGT 300
 GACTTTTTTG AACTATGTTT AGCAATACAC CAAGCCCTTT AACGATATTT CTTCAGTGCT 360
 AGCTGAGTTG CAAAGTGCTC TGGCTTGCGT AGAGCGTATC TATGGAGTCT TAGATAGCCC 420
 TGAAGTGGCT GAAACAGGTA AGGAAGTCTT GACGACCACT GACCAAGTTA AGGGAGCTAT 480
 TTCCTTTAAA CATGTCTCTT TTGGCTACCA TCCTGAAAAA ATTTTGATTA AGGACTTGTC 540
 TATCGATATT CCAGCTGGTA GTAAGGTAGC CATCGTTGGT CCGACAGGTG CTGGAAAATC 600
 AACTCTTATC AATCTCCTTA TGCCTTTTTT TCCCATTAGC TCGGGAGATA TCTTGCTGGA 660
 TGGGCAATCC ATTTATGATT ATACACGAGT ATCATTGAGA CAGCAGTTTG GTATGGTGCT 720

TCAAGAAACC TGGCTCACAC AAGGGACCAT TCATGATAAT ATTGCCTTTG GCAATCCTGA 780
 AGCCAGTCGA GAGCAAGTAA TTGCTGCTGC CAAAGCAGCT AATGCAGACT TTTTCATCCA 840
 ACAGTTGCCA CAGGGATACG ATACCAAGTT GGAAAATGCT GGAGAATCTC TCTCTGTCGG 900
 CCAAGCTCAG CTCTTGACCA TAGCCCGAGT CTTTCTGGCT ATTCCAAAGA TTCTTATCTT 960
 AGACGAGGCA ACTTCTTCCA TTGATACACG GACAGAAGTG CTGGTACAGG ATGCCTTTGC 1020
 AAAACTCATG AAGGGCCGCA CAAGTTTCAT CATTGCTCAC CGTTTGTCAG CCATTCAGGA 1080
 TGCGGATTTA ATTCTGTGCT TAGTAGATGG TGATATTGTT GAATATGGTA ACCATCAAGA 1140
 ACTCATGGAT AGAAAGGGTA AGTATTACCA AATGCAAAAA GCTGCGGCTT TTAGTTCTGA 1200
 A 1201

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Lys Lys Ser Tyr His Leu Phe Gln Lys Gln Thr Glu Thr Arg Gly Ile
 1 5 10 15
 Gln Thr Gln Leu Ile Glu Glu Ser Leu Ser Gln Gln Thr Ile Ile Gln
 20 25 30
 Ser Phe Asn Ala Gln Thr Glu Phe Ile Gln Arg Leu Arg Glu Ala His
 35 40 45
 Asp Asn Tyr Ser Gly Tyr Ser Gln Ser Ala Ile Phe Tyr Ser Ser Thr
 50 55 60
 Val Asn Pro Ser Thr Arg Phe Val Asn Ala Leu Ile Tyr Ala Leu Leu
 65 70 75 80
 Ala Gly Val Gly Ala Tyr Arg Ile Met Met Gly Ser Ala Leu Thr Val
 85 90 95
 Gly Arg Leu Val Thr Phe Leu Asn Tyr Val Gln Gln Tyr Thr Lys Pro
 100 105 110
 Phe Asn Asp Ile Ser Ser Val Leu Ala Glu Leu Gln Ser Ala Leu Ala
 115 120 125
 Cys Val Glu Arg Ile Tyr Gly Val Leu Asp Ser Pro Glu Val Ala Glu
 130 135 140
 Thr Gly Lys Glu Val Leu Thr Thr Ser Asp Gln Val Lys Gly Ala Ile
 145 150 155 160

Ser Phe Lys His Val Ser Phe Gly Tyr His Pro Glu Lys Ile Leu Ile
 165 170 175
 Lys Asp Leu Ser Ile Asp Ile Pro Ala Gly Ser Lys Val Ala Ile Val
 180 185 190
 Gly Pro Thr Gly Ala Gly Lys Ser Thr Leu Ile Asn Leu Leu Met Arg
 195 200 205
 Phe Tyr Pro Ile Ser Ser Gly Asp Ile Leu Leu Asp Gly Gln Ser Ile
 210 215 220
 Tyr Asp Tyr Thr Arg Val Ser Leu Arg Gln Gln Phe Gly Met Val Leu
 225 230 235 240
 Gln Glu Thr Trp Leu Thr Gln Gly Thr Ile His Asp Asn Ile Ala Phe
 245 250 255
 Gly Asn Pro Glu Ala Ser Arg Glu Gln Val Ile Ala Ala Ala Lys Ala
 260 265 270
 Ala Asn Ala Asp Phe Phe Ile Gln Gln Leu Pro Gln Gly Tyr Asp Thr
 275 280 285
 Lys Leu Glu Asn Ala Gly Glu Ser Leu Ser Val Gly Gln Ala Gln Leu
 290 295 300
 Leu Thr Ile Ala Arg Val Phe Leu Ala Ile Pro Lys Ile Leu Ile Leu
 305 310 315 320
 Asp Glu Ala Thr Ser Ser Ile Asp Thr Arg Thr Glu Val Leu Val Gln
 325 330 335
 Asp Ala Phe Ala Lys Leu Met Lys Gly Arg Thr Ser Phe Ile Ile Ala
 340 345 350
 His Arg Leu Ser Thr Ile Gln Asp Ala Asp Leu Ile Leu Val Leu Val
 355 360 365
 Asp Gly Asp Ile Val Glu Tyr Gly Asn His Gln Glu Leu Met Asp Arg
 370 375 380
 Lys Gly Lys Tyr Tyr Gln Met Gln Lys Ala Ala Ala Phe Ser Ser Glu
 385 390 395 400

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

ACGAAATGCA GGCAGACAG ATGCCTCGCA AATTGAAAAG GCGGCAGTTA GCCAAGGAGG	60
AAAAGCACTG AAAAAACAG AAATTAGTAA AGACGCAGAC TTGCACGAAA TTTATCTAGC	120
TGGAGGTTGT TTCTGGGGAG TGGAGGAATA TTTCTCACGT GTTCCCGGGG TGACGGATGC	180

CGTTTCAGGC TATGCAAATG GTAGAGGAGA AACAAACCAAG TACGAATTGA TTAACCAAAC 240
 AGGTCATGCA GAAACCGTCC ATGTCACCTA TGATGCCAAG CAAATTTCTC TCAAGGAAAT 300
 CCTGCTTCAC TATTTCCGCA TTATCAATCC AACCAGCAAA AATAACAAG GAAATGATGT 360
 GGGGACCCAG TACCGTACTG GTGTTTATTA CACAGATGAC AAGGATTTGG AAGTGATTAA 420
 CCAAGTCTTT GATGAGGTGG CTAAGAAATA CGATCAACCT CTAGCAGTTG AAAAGGAAAA 480
 CTTGAAGAAT TTTGTGGTGG CTGAGGATTA CCATCAAGAC TATCTCAAGA AAAATCCAAA 540
 TGGCTACTGC CATATCAATG TTAATCAGGC GGCCTATCCT GTCATTGATG CCAGCAAATA 600
 TCCAAAACCA AGTGATGAGG AATTGAAAAA GACCCTGTCA CCTGAGGAGT ATGCAGTTAC 660
 CCAGGAAAAT CAAACAGAAC GAGCTTTCTC AAACCGTTAC TGGGATAAAT TTGAATCCGG 720
 TATCTATGTG GATATAGCAA CTGGGGAACC TCTCTTTTCA TCAAAAGACA AATTTGAGTC 780
 TGGTTGTGGC TGGCCTAGTT TTACCCAACC CATCAGTCCA GATGTTGTCA CCTACAAGGA 840
 AGATAAGTCC TACAATATGA CGCGTATGGA AGTGCGGAGC CGAGTAGGAG ATTCTCACCT 900
 TGGGCATGTC TTTACGGATG GTCCACAGGA CAAGGGCGGC TTACGTTACT GTATCAATAG 960
 CCTCTCTATC CGCTTTATTC CCAAAGACCA AATGGAAGAA AAAGGCTACG CTTATTTACT 1020
 AGATTATGTT GAT 1033

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Arg Asn Ala Gly Gln Thr Asp Ala Ser Gln Ile Glu Lys Ala Ala Val
 1 5 10 15
 Ser Gln Gly Gly Lys Ala Val Lys Lys Thr Glu Ile Ser Lys Asp Ala
 20 25 30
 Asp Leu His Glu Ile Tyr Leu Ala Gly Gly Cys Phe Trp Gly Val Glu
 35 40 45
 Glu Tyr Phe Ser Arg Val Pro Gly Val Thr Asp Ala Val Ser Gly Tyr
 50 55 60
 Ala Asn Gly Arg Gly Glu Thr Thr Lys Tyr Glu Leu Ile Asn Gln Thr
 65 70 75 80
 Gly His Ala Glu Thr Val His Val Thr Tyr Asp Ala Lys Gln Ile Ser
 85 90 95

Leu Lys Glu Ile Leu Leu His Tyr Phe Arg Ile Ile Asn Pro Thr Ser
 100 105 110
 Lys Asn Lys Gln Gly Asn Asp Val Gly Thr Gln Tyr Arg Thr Gly Val
 115 120 125
 Tyr Tyr Thr Asp Asp Lys Asp Leu Glu Val Ile Asn Gln Val Phe Asp
 130 135 140
 Glu Val Ala Lys Lys Tyr Asp Gln Pro Leu Ala Val Glu Lys Glu Asn
 145 150 155 160
 Leu Lys Asn Phe Val Val Ala Glu Asp Tyr His Gln Asp Tyr Leu Lys
 165 170 175
 Lys Asn Pro Asn Gly Tyr Cys His Ile Asn Val Asn Gln Ala Ala Tyr
 180 185 190
 Pro Val Ile Asp Ala Ser Lys Tyr Pro Lys Pro Ser Asp Glu Glu Leu
 195 200 205
 Lys Lys Thr Leu Ser Pro Glu Glu Tyr Ala Val Thr Gln Glu Asn Gln
 210 215 220
 Thr Glu Arg Ala Phe Ser Asn Arg Tyr Trp Asp Lys Phe Glu Ser Gly
 225 230 235 240
 Ile Tyr Val Asp Ile Ala Thr Gly Glu Pro Leu Phe Ser Ser Lys Asp
 245 250 255
 Lys Phe Glu Ser Gly Cys Gly Trp Pro Ser Phe Thr Gln Pro Ile Ser
 260 265 270
 Pro Asp Val Val Thr Tyr Lys Glu Asp Lys Ser Tyr Asn Met Thr Arg
 275 280 285
 Met Glu Val Arg Ser Arg Val Gly Asp Ser His Leu Gly His Val Phe
 290 295 300
 Thr Asp Gly Pro Gln Asp Lys Gly Gly Leu Arg Tyr Cys Ile Asn Ser
 305 310 315 320
 Leu Ser Ile Arg Phe Ile Pro Lys Asp Gln Met Glu Glu Lys Gly Tyr
 325 330 335
 Ala Tyr Leu Leu Asp Tyr Val Asp
 340

(2) INFORMATION FOR SEQ ID NO: 193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

TGTATAGTTT TTAGCGCTTG TTCTTCTAAT TCTGNTAAAA ATGAAGAAAA TACTTCTAAA 60
 GAGCATGCCG CTGATAAAAT AGTTTTAGAT CATGCTTTTCG GTCAAACATAT ATTAGATAAA 120

AAACCTGAAA GAGTTGCAAC TATTGCTTGG GGAAATCATG ATGTAGCATT AGCTTTAGGA 180
 ATAGTTCCTG TTGGATTTTC AAAAGCAAAT TACGGTGTAAG GTGCTGATAA AGGAGTTTTA 240
 CCATGGACAG AAGAAAAAAT CAAAGAACTA AATGGTAAAG CTAACCTATT TGACGATTTG 300
 GATGGACTTA ACTTTGAAGC AATATCAAAT TCTAAACCAG ATGTTATCTT AGCAGGTTAT 360
 TCTGGTATAA CTAAAGAAGA TTATGACACT CTATCA 396

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Cys Ile Val Phe Ser Ala Cys Ser Ser Asn Ser Xaa Lys Asn Glu Glu
 1 5 10 15
 Asn Thr Ser Lys Glu His Ala Pro Asp Lys Ile Val Leu Asp His Ala
 20 25 30
 Phe Gly Gln Thr Ile Leu Asp Lys Lys Pro Glu Arg Val Ala Thr Ile
 35 40 45
 Ala Trp Gly Asn His Asp Val Ala Leu Ala Leu Gly Ile Val Pro Val
 50 55 60
 Gly Phe Ser Lys Ala Asn Tyr Gly Val Ser Ala Asp Lys Gly Val Leu
 65 70 75 80
 Pro Trp Thr Glu Glu Lys Ile Lys Glu Leu Asn Gly Lys Ala Asn Leu
 85 90 95
 Phe Asp Asp Leu Asp Gly Leu Asn Phe Glu Ala Ile Ser Asn Ser Lys
 100 105 110
 Pro Asp Val Ile Leu Ala Gly Tyr Ser Gly Ile Thr Lys Glu Asp Tyr
 115 120 125
 Asp Thr Leu Ser
 130

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

GTGTGTCGAG CATATTCTGA AGCAAACCTA TCAAAATATA GAAATTATTT TAGTTGATGA 60
 CGGTTCTACG GATAATTCTG GGGAAATTG TGATGCTTTT ATGATGCAAG ATAATCGTGT 120
 GCGAGTATTG CATCAAGAAA ATAAGGGGGG GGCAGCACAA GCTAAAAATA TGGGGATTAG 180
 TGTAGCTAAG GGAGACTACA TCACGATTGT TGATTCAGAT GATATCGTAA AAGAAAATAT 240
 GATTGAACT CTTTATCAGC AAGTCCAAGA AAAGGATGCA GATGTTGTTA TAGGGAATTA 300
 CTATAATTAT GACGAAAGTG ACGGGAATTT TTATTTTAT GTAACAGGGC AAGATTTTTG 360
 CGTCGAAGAA TTAGCTATAC AAGAAATTAT GAACCGTCAA GCAGGAGATT GGAAATTCAA 420
 TAGCTCGGCC TTTATATTGC CGACATTTAA GTTGATTAAA AAAGAATTAT TCAATGAAGT 480
 TCACTTTTCA AATGGTCGCC GCTTTGATGA TGAAGCAACT ATGCATCGCT TTTATCTTTT 540
 AGCCTCTAAA ATCGTCTTTA TAAACGATAA TCTCTATCTG TATAGAAGAC GTTCAGGAAG 600
 CATCATGAGA ACGGAATTTG ATCTTTCCTG GGCAAGAGAT ATTGTTGAAG TGTMTCTAA 660
 GAAAATATCG GATTGTGTCT TGGCTGGTTT GGATGTCTCC GTTCTGCGTA TTCGATTGT 720
 CAATCTTTTA AAAGATTATA AGCAAATTT AGAATACCAT CAATTAACAG AACTGAGGA 780
 ATATAAGAT ATTTGTTTCA GATTAAAGTT GTTTTGTGAT GCAGAACAAA GAAATGGTAA 840
 AAGT 844

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 281 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Cys Val Glu His Ile Leu Lys Gln Thr Tyr Gln Asn Ile Glu Ile Ile
 1 5 10 15
 Leu Val Asp Asp Gly Ser Thr Asp Asn Ser Gly Glu Ile Cys Asp Ala
 20 25 30
 Phe Met Met Gln Asp Asn Arg Val Arg Val Leu His Gln Glu Asn Lys
 35 40 45
 Gly Gly Ala Ala Gln Ala Lys Asn Met Gly Ile Ser Val Ala Lys Gly
 50 55 60
 Glu Tyr Ile Thr Ile Val Asp Ser Asp Asp Ile Val Lys Glu Asn Met
 65 70 75 80
 Ile Glu Thr Leu Tyr Gln Gln Val Gln Glu Lys Asp Ala Asp Val Val

85 90 95

Ile Gly Asn Tyr Tyr Asn Tyr Asp Glu Ser Asp Gly Asn Phe Tyr Phe
100 105 110

Tyr Val Thr Gly Gln Asp Phe Cys Val Glu Glu Leu Ala Ile Gln Glu
115 120 125

Ile Met Asn Arg Gln Ala Gly Asp Trp Lys Phe Asn Ser Ser Ala Phe
130 135 140

Ile Leu Pro Thr Phe Lys Leu Ile Lys Lys Glu Leu Phe Asn Glu Val
145 150 155 160

His Phe Ser Asn Gly Arg Arg Phe Asp Asp Glu Ala Thr Met His Arg
165 170 175

Phe Tyr Leu Leu Ala Ser Lys Ile Val Phe Ile Asn Asp Asn Leu Tyr
180 185 190

Leu Tyr Arg Arg Arg Ser Gly Ser Ile Met Arg Thr Glu Phe Asp Leu
195 200 205

Ser Trp Ala Arg Asp Ile Val Glu Val Phe Ser Lys Lys Ile Ser Asp
210 215 220

Cys Val Leu Ala Gly Leu Asp Val Ser Val Leu Arg Ile Arg Phe Val
225 230 235 240

Asn Leu Leu Lys Asp Tyr Lys Gln Thr Leu Glu Tyr His Gln Leu Thr
245 250 255

Asp Thr Glu Glu Tyr Lys Asp Ile Cys Phe Arg Leu Lys Leu Phe Phe
260 265 270

Asp Ala Glu Gln Arg Asn Gly Lys Ser
275 280

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

GTGTTTGGAT AGCATTCAGA ATCAGACGTA TCAAAATTTT GAGTGTATTAT TAATCAATGA 60

TGGCTCTCCA GATCATTCAT CCAAAATATG TGAAGAATTT GTAGAGAAAG ATTCTCGTTT 120

CAAATATTTT GAGAAAGCAA ACGGCGGTCT TTCATCAGCT CGTAACCTAG GTATTGAATG 180

TTCGGGGGGG GCGTACATTA CTTTGTAGA CTCTGATGAT TGGTTGGAAC ATGATGCTTT 240

AGACCGATTA TATGGTGCTT TGAAAAAGGA AAACGCAGAT ATTAGTATCG GCGTTATAA 300

TTCTTATGAT GAAACACGCT ATGTGTATAT GACTTATGTT ACGGATCCAG ATGATTCTCT 360

AGAAGTGATA GAAGGTAAAG CAATTATGGA TAGGGAAGGT GTCGAAGAAG TCAGAAATGG 420

GAACTGGACT GTAGCTGTCT TGAAGTTATT CAAGAGAGAG TTACTACAAG ATTTACCATT 480
 TCCTATAGGA AAAATGTCAG AGGATACTTA CTGGACATGG AAGGTACTTC TAAGAGCTTC 540
 GAGGATAGTC TATTTGAATC GTTGTGTTTA CTGGTACCGT GTTGGTTTAT CTGATACTTT 600
 ATCGAATACA TGGAGTGAAA AGCGTATGTA TGATGAAATT GGGGCTAGGG AAGAAAAGAT 660
 AGCTATTTTA GCAAGTTCAG ACTATGACTT GACCAATCAT ATTTTGATTT ATAAAAATAG 720
 ATTACAAAGA GTGATAGCAA AATTAGAAGA ACAAATATG CAGTTCACAG AGATTTACAG 780
 AAGAATGATG GAAAAATTGT CTTTACTTCC G 811

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Cys Leu Asp Ser Ile Gln Asn Gln Thr Tyr Gln Asn Phe Glu Cys Leu
 1 5 10 15
 Leu Ile Asn Asp Gly Ser Pro Asp His Ser Ser Lys Ile Cys Glu Glu
 20 25 30
 Phe Val Glu Lys Asp Ser Arg Phe Lys Tyr Phe Glu Lys Ala Asn Gly
 35 40 45
 Gly Leu Ser Ser Ala Arg Asn Leu Gly Ile Glu Cys Ser Gly Gly Ala
 50 55 60
 Tyr Ile Thr Phe Val Asp Ser Asp Asp Trp Leu Glu His Asp Ala Leu
 65 70 75 80
 Asp Arg Leu Tyr Gly Ala Leu Lys Lys Glu Asn Ala Asp Ile Ser Ile
 85 90 95
 Gly Arg Tyr Asn Ser Tyr Asp Glu Thr Arg Tyr Val Tyr Met Thr Tyr
 100 105 110
 Val Thr Asp Pro Asp Asp Ser Leu Glu Val Ile Glu Gly Lys Ala Ile
 115 120 125
 Met Asp Arg Glu Gly Val Glu Glu Val Arg Asn Gly Asn Trp Thr Val
 130 135 140
 Ala Val Leu Lys Leu Phe Lys Arg Glu Leu Leu Gln Asp Leu Pro Phe
 145 150 155 160
 Pro Ile Gly Lys Ile Ala Glu Asp Thr Tyr Trp Thr Trp Lys Val Leu
 165 170 175

Leu Arg Ala Ser Arg Ile Val Tyr Leu Asn Arg Cys Val Tyr Trp Tyr
 180 185 190
 Arg Val Gly Leu Ser Asp Thr Leu Ser Asn Thr Trp Ser Glu Lys Arg
 195 200 205
 Met Tyr Asp Glu Ile Gly Ala Arg Glu Glu Lys Ile Ala Ile Leu Ala
 210 215 220
 Ser Ser Asp Tyr Asp Leu Thr Asn His Ile Leu Ile Tyr Lys Asn Arg
 225 230 235 240
 Leu Gln Arg Val Ile Ala Lys Leu Glu Glu Gln Asn Met Gln Phe Thr
 245 250 255
 Glu Ile Tyr Arg Arg Met Met Glu Lys Leu Ser Leu Leu Pro
 260 265 270

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2023 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

GTGCCTAGAT AGTATTATTA CTCAACATA TAAAAATATT GAGATTGTTG TCGTTAATGA 60
 TGGTTCTACG GATGCTTCAG GTGAAATTTG TAAAGAATTT TCAGAAATGG ATCACCGAAT 120
 TCTCTATATA GAACAAGAAA ATGCTGGTCT TTCTGCCGCA CGAAACACCG GTCTGAATAA 180
 TATGTCCGGA AATTATGTGA CCTTTGTGGA CTCGGATGAT TGGATTGAGC AAGATTATGT 240
 AGAAACTCTA TATAAAAAAA TAGTAGAGTA TCAGGCTGAT ATTGCAGTTG GTAATTATTA 300
 TTCTTTCAAC GAAAGTGAAG GAATGTTCTA CTTCATATA TTGGGAGACT CCTATTATGA 360
 GAAAGTATAT GATAATGTTT CTATCTTTGA GAACTTGTAT GAAACTCAAG AAATGAAGAG 420
 TTTTGCTTTG ATATCTGCTT GGGGTAAACT CTATAAGGCA AGATTGTTTG AGCAGTTGCG 480
 CTTTGACATA GGTAAATTAG GAGAAGATGG TTACCTCAAT CAAAAGGTAT ATTTATTATC 540
 AGAAAAGGTA ATTTATTTAA ATAAAAGTCT TTATGCTTAT CGGATTAGAA AAGGTAGTTT 600
 ATCAAGAGTT TGGACAGAAA AGTGGATGCA CGCTTTAGTT GATGCTATGT CTGAACGTAT 660
 TACGCTACTA GCTAATATGG GTTATCCTCT AGAGAAACAC TTGGCAGTTT ATCGTCAGAT 720
 GTTGAAGTC AGTCTCGCCA ACGGTCAAGC TAGTGGTTTA TCTGACACAG CAACGTATAA 780
 AGAGTTTGAA ATGAAACAAA GGCTTTTAAA TCAGCTATCG AGACAAGAGG AAAGTGAAAA 840
 GAAAGCCATT GTCCTCGCAG CAACTATGG CTATGTAGAC CAAGTTTAA CGACAATCAA 900
 GTCTATTTGT TATCATAATC GTTCGATTCG TTTTATCTG ATTCATAGCG ATTTTCCAAA 960
 TGAATGGATT AAGCAATTAA ATAAGCGCTT AGAGAAGTTT GACTCAGAAA TTATTAATTG 1020

TCGGGTAAC TCTGAGCAAA TTTCATGTTA TAAATCGGAT ATTAGTTACA CAGTCTTTTT 1080
 ACGCTATTC ATAGCTGATT TCGTGCAAGA AGACAAGGCC CTCTACTTGG ACTGTGATCT 1140
 AGTTGTAACG AAAAATCTGG ATGACTTGTT TGCTACAGAC TTACAAGATT ATCCTTTGGC 1200
 TGCTGTTAGA GATTTTGGGG GCAGAGCTTA TTTTGGTCAA GAAATCTTTA ATGCCGGTGT 1260
 TCTCTTGGTA AACAAATGCTT TTTGGAAAAA AGAGAATATG ACCCAAAAAT TAATTGATGT 1320
 AACCAATGAA TGGCATGATA AGGTGGATCA GGCAGATCAG AGCATCTTGA ATATGCTTTT 1380
 TGAACATAAA TGGTTGGAAT TGGACTTTGA TTATAATCAT ATTGTCATTC ATAAACAGTT 1440
 TGCTGATTAT CAATTGCCTG AGGGTCAGGA TTATCTGCT ATTATTCACT ATCTTTCTCA 1500
 TCGGAAACCG TGGAAAGATT TGGCGGCCCA AACCTATCGT GAAGTTTGGT GGTACTATCA 1560
 TGGGCTTGAA TGGACAGAAT TGGGACAAAA CCATCATTTA CATCCATTAC AAAGATCTCA 1620
 CATCTATCCA ATAAAGGAAC CTTTCACTTG TCTAATCTAT ACTGCCTCAG ACCATATTGA 1680
 ACAAATTGAG ACATTGGTTC AATCCTTGCC TGATATTCAG TTTAAGATAG CAGCTAGAGT 1740
 AATAGTTAGT GATCGATTGG CTCAGATGAC AATTTATCCA AACGTGACTA TATTTAACGG 1800
 AATTCATAT TTGGTAGATG TCGATAATGA ATTTGGTAGAA ACCAGTCAAG TACTTTTAGA 1860
 TATTAATCAT GGCGAAAAGA CAGAAGAAAT TCTCGATCAA TTTGCTAATC TTGGCAAGCC 1920
 TATCTTATCC TTTGAAAATA CTAAACCTA TGAAGTAGGT CAGGAGGCAT ATGCTGTTGA 1980
 CCAAGTTCAA GCAATGATTG AAAAATTGAG AGAAATAAGC AAA 2023

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 674 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Cys Leu Asp Ser Ile Ile Thr Gln Thr Tyr Lys Asn Ile Glu Ile Val
 1 5 10 15
 Val Val Asn Asp Gly Ser Thr Asp Ala Ser Gly Glu Ile Cys Lys Glu
 20 25 30
 Phe Ser Glu Met Asp His Arg Ile Leu Tyr Ile Glu Gln Glu Asn Ala
 35 40 45
 Gly Leu Ser Ala Ala Arg Asn Thr Gly Leu Asn Asn Met Ser Gly Asn
 50 55 60
 Tyr Val Thr Phe Val Asp Ser Asp Asp Trp Ile Glu Gln Asp Tyr Val

307

405 410 415
 Asn Ala Gly Val Leu Leu Val Asn Asn Ala Phe Trp Lys Lys Glu Asn
 420 425 430
 Met Thr Gln Lys Leu Ile Asp Val Thr Asn Glu Trp His Asp Lys Val
 435 440 445
 Asp Gln Ala Asp Gln Ser Ile Leu Asn Met Leu Phe Glu His Lys Trp
 450 455 460
 Leu Glu Leu Asp Phe Asp Tyr Asn His Ile Val Ile His Lys Gln Phe
 465 470 475 480
 Ala Asp Tyr Gln Leu Pro Glu Gly Gln Asp Tyr Pro Ala Ile Ile His
 485 490 495
 Tyr Leu Ser His Arg Lys Pro Trp Lys Asp Leu Ala Ala Gln Thr Tyr
 500 505 510
 Arg Glu Val Trp Trp Tyr Tyr His Gly Leu Glu Trp Thr Glu Leu Gly
 515 520 525
 Gln Asn His His Leu His Pro Leu Gln Arg Ser His Ile Tyr Pro Ile
 530 535 540
 Lys Glu Pro Phe Thr Cys Leu Ile Tyr Thr Ala Ser Asp His Ile Glu
 545 550 555 560
 Gln Ile Glu Thr Leu Val Gln Ser Leu Pro Asp Ile Gln Phe Lys Ile
 565 570 575
 Ala Ala Arg Val Ile Val Ser Asp Arg Leu Ala Gln Met Thr Ile Tyr
 580 585 590
 Pro Asn Val Thr Ile Phe Asn Gly Ile His Tyr Leu Val Asp Val Asp
 595 600 605
 Asn Glu Leu Val Glu Thr Ser Gln Val Leu Leu Asp Ile Asn His Gly
 610 615 620
 Glu Lys Thr Glu Glu Ile Leu Asp Gln Phe Ala Asn Leu Gly Lys Pro
 625 630 635 640
 Ile Leu Ser Phe Glu Asn Thr Lys Thr Tyr Glu Val Gly Gln Glu Ala
 645 650 655
 Tyr Ala Val Asp Gln Val Gln Ala Met Ile Glu Lys Leu Arg Glu Ile
 660 665 670
 Ser Lys

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

CATTGAGAAG CAGACCTATC AAAATCTGGA AATTATTCTT GTTGATGATG GTGCAACAGA 60
 TGAAAGTGGT CGCTTGTGTG ATTCAATCGC TGAACAAGAT GACAGGGTGT CAGTGCTTCA 120
 TAAAAAGAAC GAAGGATTGT CGCAAGCAGC AAATGATGGG ATGAAGCAGG CTCACGGGGA 180
 TTATCTGATT TTTATTGACT CAGATGATTA TATCCATCCA GAAATGATTC AGAGCTTATA 240
 TGAGCAATTA GTTCAAGAAG ATGCGGATGT TTCGAGCTGT GGTGTCATGA ATGTCTATGC 300
 TAATGATGAA AGCCACAGT CAGCCAATCA GGATGACTAT TTTGTCTGTG ATTCTCAAAC 360
 ATTTCTAAAG GAATACCTCA TAGGTGAAAA AATACCTGGG ACGATTGCA ATAAGCTAAT 420
 CAAGAGACAG ATTGCAACTG CCCTATCCTT TCCTAAGGGG TTGATTTACG AAGATGCCTA 480
 TTACCATTTT GATTTAATCA AGTTGGCCAA GAAGTATGTG GTTAATACTA AACCCATTA 540
 TTACTATTTT CATAGAGGGG ATAGTATTAC GACCAAACCC TATGCAGAGA AGGATTTAGC 600
 CTATATTGAT ATCTACCAA AGTTTTATAA TGAAGTTGTG AAAAATATC CTGACTTGAA 660
 AGAGGTCGCT TTTTTCAGAT TGGCCTATGC CCACTTCTTT ATTCTGGATA AGATGTTGCT 720
 AGATGATCAG TATAAACAGT TTGAAGCCTA TTCTCAGATT CATCGTMTT TAAAAGGCCA 780
 TGCCTTTGCT ATTTCTAGGA ATCCAATTTT CCGTAAGGGG AGAAGAATTA GTGCTTTGGC 840
 CCTATTCATA AATATTTTCT TATATCGATT CTTATTACTG AAAAATATTG AAAAATCTAA 900
 AAAATTACAT 910

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Ile Gln Lys Gln Thr Tyr Gln Asn Leu Glu Ile Ile Leu Val Asp Asp
 1 5 10 15
 Gly Ala Thr Asp Glu Ser Gly Arg Leu Cys Asp Ser Ile Ala Glu Gln
 20 25 30
 Asp Asp Arg Val Ser Val Leu His Lys Lys Asn Glu Gly Leu Ser Gln
 35 40 45
 Ala Arg Asn Asp Gly Met Lys Gln Ala His Gly Asp Tyr Leu Ile Phe
 50 55 60
 Ile Asp Ser Asp Asp Tyr Ile His Pro Glu Met Ile Gln Ser Leu Tyr
 65 70 75 80

Glu Gln Leu Val Gln Glu Asp Ala Asp Val Ser Ser Cys Gly Val Met
 85 90 95
 Asn Val Tyr Ala Asn Asp Glu Ser Pro Gln Ser Ala Asn Gln Asp Asp
 100 105 110
 Tyr Phe Val Cys Asp Ser Gln Thr Phe Leu Lys Glu Tyr Leu Ile Gly
 115 120 125
 Glu Lys Ile Pro Gly Thr Ile Cys Asn Lys Leu Ile Lys Arg Gln Ile
 130 135 140
 Ala Thr Ala Leu Ser Phe Pro Lys Gly Leu Ile Tyr Glu Asp Ala Tyr
 145 150 155 160
 Tyr His Phe Asp Leu Ile Lys Leu Ala Lys Lys Tyr Val Val Asn Thr
 165 170 175
 Lys Pro Tyr Tyr Tyr Tyr Phe His Arg Gly Asp Ser Ile Thr Thr Lys
 180 185 190
 Pro Tyr Ala Glu Lys Asp Leu Ala Tyr Ile Asp Ile Tyr Gln Lys Phe
 195 200 205
 Tyr Asn Glu Val Val Lys Asn Tyr Pro Asp Leu Lys Glu Val Ala Phe
 210 215 220
 Phe Arg Leu Ala Tyr Ala His Phe Phe Ile Leu Asp Lys Met Leu Leu
 225 230 235 240
 Asp Asp Gln Tyr Lys Gln Phe Glu Ala Tyr Ser Gln Ile His Arg Phe
 245 250 255
 Leu Lys Gly His Ala Phe Ala Ile Ser Arg Asn Pro Ile Phe Arg Lys
 260 265 270
 Gly Arg Arg Ile Ser Ala Leu Ala Leu Phe Ile Asn Ile Ser Leu Tyr
 275 280 285
 Arg Phe Leu Leu Leu Lys Asn Ile Glu Lys Ser Lys Lys Leu His
 290 295 300

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

TAAGGCTGAT AATCGTGTTC AAATGAGAAC GACGATTAAT AATGAATCGC CATTGTTGCT 60
 TTCTCCGTTG TATGGCAATG ATAATGGTAA CGGATTATGG TGGGGAACA CATTGAAGGG 120
 AGCATGGGAA GCTATTCCTG AAGATGTAAA GCCATATGCA GCGATTGAAC TTCATCCTGC 180
 AAAAGTCTGT AAACCAACAA GTTGATTCC ACGAGATACG AAAGAATTGA GAGAATGGTA 240

TGTCAAGATG TTGGAGGAAG CTCAAAGTCT AAACATTCCA GTTTTCTTGG TTATTATGTC 300
 GGCTGGAGAG CGTAATACAG TTCCTCCAGA GTGGTTAGAT GAACAATTCC AAAAGTATAG 360
 TGTGTTAAAA GGTGTTTTAA ATATTGAGAA TTATTGGATT TACAATAACC AGTTAGCTCC 420
 GCATAGTGCT AAATATTTGG AAGTTTGTGC CAAATATGGA GCGCATTTTA TCTGGCATGA 480
 TCATGAAAAA TGGTTCCTGGG AAACATTAT GAATGATCCG ACATTCTTTG AAGCGAGTCA 540
 AAAATATCAT AAAAATTTGG TGTGCGCAAC TAAAAATACG CCAATAAGAG ATGATGCGGG 600
 TACAGATTCT ATCGTTAGTG GATTTTGGTT GAGTGGCTTA TGTGATAACT GGGGCTCATC 660
 AACAGATACA TGGAAATGGT GGGAAAAACA TTATACAAAC ACATTTGAAA CTGGAAGAGC 720
 TAGGGATATG AGATCCTATG CATCGGAACC AGAATCAATG ATTGCTATGG AAATGATGAA 780
 TGTATATACT GGGGAGGCA CAGTTTATAA TTTCGAATGT GCCGCGTATA CATTTATGAC 840
 AAATGATGTA CCAACTCCAG CATTTACTAA AGGTATTATT CCTTTCCTTA GACATGCTAT 900
 ACAAATCCA GCTCCAAGTA AGGAAGAAGT TGTAAATAGA ACAAAGCTG TATTTTGGAA 960
 TGGAGAAGGT AGGATTAGTT CATTAAACGG ATTTTATCAA GGACTTTATT CGAATGATGA 1020
 AACAATGCCT TTATATAATA ATGGGAGATA TCATATCTT CCTGTAATAC ATGAGAAAAT 1080
 TGATAAGGAA AAGATTTTAT CTATATTTCC TAATGCAAAA ATTTTGACTA AAAATAGTGA 1140
 GGAATTGTCT AGTAAAGTCA ACTATTTAAA CTCGCTTTAT CCAAACTTT ATGAAGGAGA 1200
 TGGGTATGCT CAGCGTGTAG GTAATTCCTG GTATATTTAT AATAGTAATG CTAATATCAA 1260
 TAAAAATCAG CAAGTAATGT TGCCTATGTA TACTAATAAT ACAAAGTCGT TATCGTTAGA 1320
 TTTGACGCCA CATACTTACG CTGTTGTTAA AGAAAATCCA AATAATTAC ATATTTTATT 1380
 GAATAATTAC AGGACAGATA AGACAGCTAT GTGGGCATTA TCAGGAAATT TTGATGCATC 1440
 AAAAAGTTGG AAGAAAGAAG AATTAGAGTT AGCGAACTGG ATAAGCAAAA ATTATTCCAT 1500
 CAATCCTGTA GATAATGACT TTAGGACAAC AACACTTACA TTAAAAGGGC ATACTGGTCA 1560
 TAAACCTCAG ATAAATATAA GTGGCGATAA AAATCATTAT ACTTATACAG AAAATTGGGA 1620
 TGAGAATACC CATGTTTATA CCATTACGGT TAATCATAAT GGAATGGTAG AGATGTCTAT 1680
 AAATACTGAG GGGACAGGTC CAGTCTCTTT CCCAACACCA GATAAATTTA ATGATGGTAA 1740
 TTTGAATATA GCATATGCAA AACCAACAAC ACAAAGTTCT GTAGATTACA ATGGAGACCC 1800
 TAATAGAGCT GTGGATGGTA ACAGAAATGG TAATTTTAACT TCTGGTTCGG TAACACACAC 1860
 TAGGGCAGAT AATCCCTCTT GGTGGGAAGT CGATTTGAAA AAAATGGATA AAGTTGGGCT 1920
 TGTAAAAATT TATAATCGCA CAGATGCTGA GACTCAACGT CTATCTAATT TT 1972

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 657 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Lys Ala Asp Asn Arg Val Gln Met Arg Thr Thr Ile Asn Asn Glu Ser
 1 5 10 15
 Pro Leu Leu Leu Ser Pro Leu Tyr Gly Asn Asp Asn Gly Asn Gly Leu
 20 25 30
 Trp Trp Gly Asn Thr Leu Lys Gly Ala Trp Glu Ala Ile Pro Glu Asp
 35 40 45
 Val Lys Pro Tyr Ala Ala Ile Glu Leu His Pro Ala Lys Val Cys Lys
 50 55 60
 Pro Thr Ser Cys Ile Pro Arg Asp Thr Lys Glu Leu Arg Glu Trp Tyr
 65 70 75 80
 Val Lys Met Leu Glu Glu Ala Gln Ser Leu Asn Ile Pro Val Phe Leu
 85 90 95
 Val Ile Met Ser Ala Gly Glu Arg Asn Thr Val Pro Pro Glu Trp Leu
 100 105 110
 Asp Glu Gln Phe Gln Lys Tyr Ser Val Leu Lys Gly Val Leu Asn Ile
 115 120 125
 Glu Asn Tyr Trp Ile Tyr Asn Asn Gln Leu Ala Pro His Ser Ala Lys
 130 135 140
 Tyr Leu Glu Val Cys Ala Lys Tyr Gly Ala His Phe Ile Trp His Asp
 145 150 155 160
 His Glu Lys Trp Phe Trp Glu Thr Ile Met Asn Asp Pro Thr Phe Phe
 165 170 175
 Glu Ala Ser Gln Lys Tyr His Lys Asn Leu Val Leu Ala Thr Lys Asn
 180 185 190
 Thr Pro Ile Arg Asp Asp Ala Gly Thr Asp Ser Ile Val Ser Gly Phe
 195 200 205
 Trp Leu Ser Gly Leu Cys Asp Asn Trp Gly Ser Ser Thr Asp Thr Trp
 210 215 220
 Lys Trp Trp Glu Lys His Tyr Thr Asn Thr Phe Glu Thr Gly Arg Ala
 225 230 235 240
 Arg Asp Met Arg Ser Tyr Ala Ser Glu Pro Glu Ser Met Ile Ala Met
 245 250 255
 Glu Met Met Asn Val Tyr Thr Gly Gly Gly Thr Val Tyr Asn Phe Glu
 260 265 270
 Cys Ala Ala Tyr Thr Phe Met Thr Asn Asp Val Pro Thr Pro Ala Phe
 275 280 285

Thr Lys Gly Ile Ile Pro Phe Phe Arg His Ala Ile Gln Asn Pro Ala
 290 295 300
 Pro Ser Lys Glu Glu Val Val Asn Arg Thr Lys Ala Val Phe Trp Asn
 305 310 315 320
 Gly Glu Gly Arg Ile Ser Ser Leu Asn Gly Phe Tyr Gln Gly Leu Tyr
 325 330 335
 Ser Asn Asp Glu Thr Met Pro Leu Tyr Asn Asn Gly Arg Tyr His Ile
 340 345 350
 Leu Pro Val Ile His Glu Lys Ile Asp Lys Glu Lys Ile Ser Ser Ile
 355 360 365
 Phe Pro Asn Ala Lys Ile Leu Thr Lys Asn Ser Glu Glu Leu Ser Ser
 370 375 380
 Lys Val Asn Tyr Leu Asn Ser Leu Tyr Pro Lys Leu Tyr Glu Gly Asp
 385 390 395 400
 Gly Tyr Ala Gln Arg Val Gly Asn Ser Trp Tyr Ile Tyr Asn Ser Asn
 405 410 415
 Ala Asn Ile Asn Lys Asn Gln Gln Val Met Leu Pro Met Tyr Thr Asn
 420 425 430
 Asn Thr Lys Ser Leu Ser Leu Asp Leu Thr Pro His Thr Tyr Ala Val
 435 440 445
 Val Lys Glu Asn Pro Asn Asn Leu His Ile Leu Leu Asn Asn Tyr Arg
 450 455 460
 Thr Asp Lys Thr Ala Met Trp Ala Leu Ser Gly Asn Phe Asp Ala Ser
 465 470 475 480
 Lys Ser Trp Lys Lys Glu Glu Leu Glu Leu Ala Asn Trp Ile Ser Lys
 485 490 495
 Asn Tyr Ser Ile Asn Pro Val Asp Asn Asp Phe Arg Thr Thr Thr Leu
 500 505 510
 Thr Leu Lys Gly His Thr Gly His Lys Pro Gln Ile Asn Ile Ser Gly
 515 520 525
 Asp Lys Asn His Tyr Thr Tyr Thr Glu Asn Trp Asp Glu Asn Thr His
 530 535 540
 Val Tyr Thr Ile Thr Val Asn His Asn Gly Met Val Glu Met Ser Ile
 545 550 555 560
 Asn Thr Glu Gly Thr Gly Pro Val Ser Phe Pro Thr Pro Asp Lys Phe
 565 570 575
 Asn Asp Gly Asn Leu Asn Ile Ala Tyr Ala Lys Pro Thr Thr Gln Ser
 580 585 590
 Ser Val Asp Tyr Asn Gly Asp Pro Asn Arg Ala Val Asp Gly Asn Arg
 595 600 605
 Asn Gly Asn Phe Asn Ser Gly Ser Val Thr His Thr Arg Ala Asp Asn
 610 615 620

Pro Ser Trp Trp Glu Val Asp Leu Lys Lys Met Asp Lys Val Gly Leu
625 630 635 640

Val Lys Ile Tyr Asn Arg Thr Asp Ala Glu Thr Gln Arg Leu Ser Asn
645 650 655

Phe

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

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CTGTGGCAAT CAGTCAGCTG CTTCCAAACA GTCAGCTTCA GGAACGATTG AGGTGATTTC	60
ACGAGAAAAT GGCTCTGGGA CACGGGGTGC CTTACAGAA ATCACAGGGA TTCTCAAAAA	120
AGACGGTGAT AAAAAAATTG ACAACACTGC CAAAACAGCT GTGATTCAAA ATAGTACAGA	180
AGGTGTCTTC TCAGCAGTTC AAGGGAATGC TAATGCTATC GGCTACATCT CCTTGGGATC	240
TTTAACGAAA TCTGTCAAGG CTTTAGAGAT TGATGGTGTG AAGGCTAGTC GAGACACAGT	300
TTTAGATGGT GAATACCTTC TTCAACGTCC CTTCAACATT GTTTGGTCTT CTAATCTTTC	360
CAAGCTAGGT CAAGATTTTA TCAGCTTTAT CCACTCCAAA CAAGGTCAAC AAGTGGTCAC	420
AGATAATAAA TTTATTGAAG CTAAAACCGA AACCACGGAA TATACAAGCC AACACTTATC	480
AGGCAAGTTG TCTGTTGTAG GTTCCACTTC AGTATCTTCT TTAATGGAAA AATTAGCAGA	540
AGCTTATAAA AAAGAAAATC CAGAAGTTAC GATTGATATT ACCTCTAATG GGTCTTCAGC	600
AGGTATTACC GCTGTTAAGG AGAAAACCGC TGATATTGGT ATGGTTTCTA GGAATTAAC	660
TCCTGAAGAA GGTAAGAGTC TCACCCATGA TGCTATTGCT TTAGACGGTA TTGCTGTTGT	720
GGTCAATAAT GACAATAAGG CAAGCCAAGT CAGTATGGCT GAACCTGCAG ACGTTTTTAG	780
TGGCAAATTA ACCACCTGGG ACAAGATTAA A	811

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Cys Gly Asn Gln Ser Ala Ala Ser Lys Gln Ser Ala Ser Gly Thr Ile
 1 5 10 15
 Glu Val Ile Ser Arg Glu Asn Gly Ser Gly Thr Arg Gly Ala Phe Thr
 20 25 30
 Glu Ile Thr Gly Ile Leu Lys Lys Asp Gly Asp Lys Lys Ile Asp Asn
 35 40 45
 Thr Ala Lys Thr Ala Val Ile Gln Asn Ser Thr Glu Gly Val Leu Ser
 50 55 60
 Ala Val Gln Gly Asn Ala Asn Ala Ile Gly Tyr Ile Ser Leu Gly Ser
 65 70 75 80
 Leu Thr Lys Ser Val Lys Ala Leu Glu Ile Asp Gly Val Lys Ala Ser
 85 90 95
 Arg Asp Thr Val Leu Asp Gly Glu Tyr Pro Leu Gln Arg Pro Phe Asn
 100 105 110
 Ile Val Trp Ser Ser Asn Leu Ser Lys Leu Gly Gln Asp Phe Ile Ser
 115 120 125
 Phe Ile His Ser Lys Gln Gly Gln Gln Val Val Thr Asp Asn Lys Phe
 130 135 140
 Ile Glu Ala Lys Thr Glu Thr Thr Glu Tyr Thr Ser Gln His Leu Ser
 145 150 155 160
 Gly Lys Leu Ser Val Val Gly Ser Thr Ser Val Ser Ser Leu Met Glu
 165 170 175
 Lys Leu Ala Glu Ala Tyr Lys Lys Glu Asn Pro Glu Val Thr Ile Asp
 180 185 190
 Ile Thr Ser Asn Gly Ser Ser Ala Gly Ile Thr Ala Val Lys Glu Lys
 195 200 205
 Thr Ala Asp Ile Gly Met Val Ser Arg Glu Leu Thr Pro Glu Glu Gly
 210 215 220
 Lys Ser Leu Thr His Asp Ala Ile Ala Leu Asp Gly Ile Ala Val Val
 225 230 235 240
 Val Asn Asn Asp Asn Lys Ala Ser Gln Val Ser Met Ala Glu Leu Ala
 245 250 255
 Asp Val Phe Ser Gly Lys Leu Thr Thr Trp Asp Lys Ile Lys
 260 265 270

(2) INFORMATION FOR SEQ ID NO: 207:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 805 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

TTGTCAACAA CAACATGCTA CTTCTGAGGG GACGAATCAA AGGCAAAGCA GTTCAGCGAA 60
 AGTTCCATGG AAAGCTTCAT ACACCAACCT AAACAACCAG GTAAGTACAG AAGAGGTCAA 120
 ATCTCTCTTA TCAGCTCACT TGGATCCAAA TAGTGTGTGAT GCATTTTMTA ATCTCGTTAA 180
 TGACTATAAT ACCATTGTCTG GCTCAACTGG CTTATCAGGA GATTTCACTT CCTTTACTCA 240
 CACCGAATAC GATGTTGAGA AAATCAGTCA TCTCTGGAAT CAAAAGAAGG GCGATTTTGT 300
 TGGGACCAAC TGCCGTATCA ATAGTTATTG TCTTTTGAAA AATTCAGTCA CCATTCCAAA 360
 GCTTGAAAAG AATGACCAGT TGCTTTTCCT AGATAATGAT GCGATTGATA AAGGAAAGGT 420
 CTTTGATTCA CAAGATAAGG AAGAGTTTGA TATTCTATTT TCGAGAGTTC CAACTGAGTC 480
 AACTACAGAT GTCAAGGTTT ACGCTGAAAA GATGGAAGCA TTCTTCTCAC AATTTCAATT 540
 CAATGAAAAA GCTCGAATGC TGTCTGTAGT CTTGCACGAC AATTTGGATG GCGAGTATCT 600
 GTTTGTAGGC CACGTTGGGG TCTTAGTACC TGCTGATGAC GGTTTCTTAT TTGTAGAGAA 660
 ATTGACTTTC GAAGAGCCCT ACCAAGCGAT TAAATTTGCT AGTAAGGAAG ATTGCTACAA 720
 GTATTTGGGC ACCAAGTATG CGGATTATAC AGGCGAGGGA CTGGCTAAGC CTTTATCAT 780
 GGATAATGAT AAGTGGGTTA AACTT 805

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Cys Gln Gln Gln His Ala Thr Ser Glu Gly Thr Asn Gln Arg Gln Ser
 1 5 10 15
 Ser Ser Ala Lys Val Pro Trp Lys Ala Ser Tyr Thr Asn Leu Asn Asn
 20 25 30
 Gln Val Ser Thr Glu Glu Val Lys Ser Leu Leu Ser Ala His Leu Asp
 35 40 45
 Pro Asn Ser Val Asp Ala Phe Phe Asn Leu Val Asn Asp Tyr Asn Thr
 50 55 60
 Ile Val Gly Ser Thr Gly Leu Ser Gly Asp Phe Thr Ser Phe Thr His
 65 70 75 80
 Thr Glu Tyr Asp Val Glu Lys Ile Ser His Leu Trp Asn Gln Lys Lys
 85 90 95

Gly Asp Phe Val Gly Thr Asn Cys Arg Ile Asn Ser Tyr Cys Leu Leu
 100 105 110
 Lys Asn Ser Val Thr Ile Pro Lys Leu Glu Lys Asn Asp Gln Leu Leu
 115 120 125
 Phe Leu Asp Asn Asp Ala Ile Asp Lys Gly Lys Val Phe Asp Ser Gln
 130 135 140
 Asp Lys Glu Glu Phe Asp Ile Leu Phe Ser Arg Val Pro Thr Glu Ser
 145 150 155 160
 Thr Thr Asp Val Lys Val His Ala Glu Lys Met Glu Ala Phe Phe Ser
 165 170 175
 Gln Phe Gln Phe Asn Glu Lys Ala Arg Met Leu Ser Val Val Leu His
 180 185 190
 Asp Asn Leu Asp Gly Glu Tyr Leu Phe Val Gly His Val Gly Val Leu
 195 200 205
 Val Pro Ala Asp Asp Gly Phe Leu Phe Val Glu Lys Leu Thr Phe Glu
 210 215 220
 Glu Pro Tyr Gln Ala Ile Lys Phe Ala Ser Lys Glu Asp Cys Tyr Lys
 225 230 235 240
 Tyr Leu Gly Thr Lys Tyr Ala Asp Tyr Thr Gly Glu Gly Leu Ala Lys
 245 250 255
 Pro Phe Ile Met Asp Asn Asp Lys Trp Val Lys Leu
 260 265

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cont.
(2) INFORMATION FOR SEQ ID NO: 209:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 508 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

TTGTTTCAGGC AAGTCCGTGA CTAGTGAACA CCAAACGAAA GATGAAATGA AGACGGAGCA	60
GACAGCTAGT AAAACAAGCG CAGCTAAAGG GAAAGAGGTG GCTGATTTTG AATTGATGGG	120
AGTAGATGGC AAGACCTACC GTTTATCTGA TTACAAGGGC AAGAAAGTCT ATCTCAAATT	180
CTGGGCTTCT TGGTGTTCCTA TCTGTCTGGC TAGTCTTCCA GATACGGATG AGATTGCTAA	240
AGAAGCTGGT GATGACTATG TGGTCTTGAC AGTAGTGTCA CCAGGACATA AGGGAGAGCA	300
ATCTGAAGCG GACTTTAAGA ATTGGTATAA GGGATTGGAT TATAAAAATC TCCCAGTCCT	360
AGTTGACCCA TCAGGCAAAC TTTTGGAAC TTATGGTGTG CGTTCTTACC CAACCCAAGC	420
CTTTATAGAC AAAGAAGGCA AGCTGGTCAA AACACATCCA GGATTCATGG AAAAAGATGC	480
AATTTTGCAA ACTTTGAAGG AATTAGCC	508

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Cys Ser Gly Lys Ser Val Thr Ser Glu His Gln Thr Lys Asp Glu Met
 1 5 10 15
 Lys Thr Glu Gln Thr Ala Ser Lys Thr Ser Ala Ala Lys Gly Lys Glu
 20 25 30
 Val Ala Asp Phe Glu Leu Met Gly Val Asp Gly Lys Thr Tyr Arg Leu
 35 40 45
 Ser Asp Tyr Lys Gly Lys Lys Val Tyr Leu Lys Phe Trp Ala Ser Trp
 50 55 60
 Cys Ser Ile Cys Leu Ala Ser Leu Pro Asp Thr Asp Glu Ile Ala Lys
 65 70 75 90
 Glu Ala Gly Asp Asp Tyr Val Val Leu Thr Val Val Ser Pro Gly His
 85 90 95
 Lys Gly Glu Gln Ser Glu Ala Asp Phe Lys Asn Trp Tyr Lys Gly Leu
 100 105 110
 Asp Tyr Lys Asn Leu Pro Val Leu Val Asp Pro Ser Gly Lys Leu Leu
 115 120 125
 Glu Thr Tyr Gly Val Arg Ser Tyr Pro Thr Gln Ala Phe Ile Asp Lys
 130 135 140
 Glu Gly Lys Leu Val Lys Thr His Pro Gly Phe Met Glu Lys Asp Ala
 145 150 155 160
 Ile Leu Gln Thr Leu Lys Glu Leu Ala
 165

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 994 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

CTCGCAAATT GAAAAGGCGG CAGTTAGCCA AGGAGGAAAA GCAGTGAAAA AACAGAAAT 60
 TAGTAAAGAC GCAGACTTGC ACGAAATTTA TCTAGCTGGA GGTGTTTCT GGGGAGTGA 120

GGAATATTTTC TCACGTGTTT CCGGGGTGAC GGATGCCGTT TCAGGCTATG CAAATGGTAG 180
 AGGAGAAACA ACCAAGTACG AATTGATTAA CCAAACAGGT CATGCAGAAA CCGTCCATGT 240
 CACCTATGAT GCCAAGCAAA TTTCTCTCAA GGAAATCCTG CTTCACTATT TCCGCATTAT 300
 CAATCCAACC AGCAAAAATA AACAAGGAAA TGATGTGGGG ACCCAGTACC GTACTGGTGT 360
 TTATTACACA GATGACAAGG ATTTGGAAGT GATTAAACCA GTCTTTGATG AGGTGGCTAA 420
 GAAATACGAT CAACCTCTAG CAGTTGAAAA GGAAGACTTG AAGAATTTTG TGGTGGCTGA 480
 GGATTACCAT CAAGACTATC TCAAGAAAAA TCCAAATGGC TACTGCCATA TCAATGTTAA 540
 TCAGGCGGCC TATCCTGTCA TTGATGCCAG CAAATATCCA AAACCAAGTG ATGAGGAATT 600
 GAAAAAGACC CTGTCACTG AGGAGTATGC AGTTACCCAG GAAATCAAA CAGAACGAGC 660
 TTTCTCAAAC CGTTACTGGG ATAAATTTGA ATCCGGTATC TATGTGGATA TAGCAACTGG 720
 GGAACCTCTC TTTTCATCAA AAGACAAATT TGAGTCTGGT TGTGGCTGGC CTAGTTTAC 780
 CCAACCCATC AGTCCAGATG TTGTCACCTA CAAGGAAGAT AAGTCTACA ATATGACGCG 840
 TATGGAAGTG CGGAGCCGAG TAGGAGATTC TCACCTTGGG CATGTCTTTA CGGATGGTCC . 900
 ACAGGACAAG GCGGCTTAC GTTACTGTAT CAATAGCCTC TCTATCCGCT TTATTCCCAA 960
 AGACCAAATG GAAGAAAAAG GTACGCTTAT TTAC 994

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 331 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Ser Gln Ile Glu Lys Ala Ala Val Ser Gln Gly Gly Lys Ala Val Lys
 1 5 10 15
 Lys Thr Glu Ile Ser Lys Asp Ala Asp Leu His Glu Ile Tyr Leu Ala
 20 25 30
 Gly Gly Cys Phe Trp Gly Val Glu Glu Tyr Phe Ser Arg Val Pro Gly
 35 40 45
 Val Thr Asp Ala Val Ser Gly Tyr Ala Asn Gly Arg Gly Glu Thr Thr
 50 55 60
 Lys Tyr Glu Leu Ile Asn Gln Thr Gly His Ala Glu Thr Val His Val
 65 70 75 80
 Thr Tyr Asp Ala Lys Gln Ile Ser Leu Lys Glu Ile Leu Leu His Tyr
 85 90 95

Phe Arg Ile Ile Asn Pro Thr Ser Lys Asn Lys Gln Gly Asn Asp Val
 100 105 110
 Gly Thr Gln Tyr Arg Thr Gly Val Tyr Tyr Thr Asp Asp Lys Asp Leu
 115 120 125
 Glu Val Ile Asn Gln Val Phe Asp Glu Val Ala Lys Lys Tyr Asp Gln
 130 135 140
 Pro Leu Ala Val Glu Lys Glu Asn Leu Lys Asn Phe Val Val Ala Glu
 145 150 155 160
 Asp Tyr His Gln Asp Tyr Leu Lys Lys Asn Pro Asn Gly Tyr Cys His
 165 170 175
 Ile Asn Val Asn Gln Ala Ala Tyr Pro Val Ile Asp Ala Ser Lys Tyr
 180 185 190
 Pro Lys Pro Ser Asp Glu Glu Leu Lys Lys Thr Leu Ser Pro Glu Glu
 195 200 205
 Tyr Ala Val Thr Gln Glu Asn Gln Thr Glu Arg Ala Phe Ser Asn Arg
 210 215 220
 Tyr Trp Asp Lys Phe Glu Ser Gly Ile Tyr Val Asp Ile Ala Thr Gly
 225 230 235 240
 Glu Pro Leu Phe Ser Ser Lys Asp Lys Phe Glu Ser Gly Cys Gly Trp
 245 250 255
 Pro Ser Phe Thr Gln Pro Ile Ser Pro Asp Val Val Thr Tyr Lys Glu
 260 265 270
 Asp Lys Ser Tyr Asn Met Thr Arg Met Glu Val Arg Ser Arg Val Gly
 275 280 285
 Asp Ser His Leu Gly His Val Phe Thr Asp Gly Pro Gln Asp Lys Gly
 290 295 300
 Gly Leu Arg Tyr Cys Ile Asn Ser Leu Ser Ile Arg Phe Ile Pro Lys
 305 310 315 320
 Asp Gln Met Glu Glu Lys Gly Thr Leu Ile Tyr
 325 330

(2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 625 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

TGTTCAGTCA GGTCTAATG GTTCTCAGTC TGCTGTGGAT GCTATCAAAC AAAAAGGGAA	60
ATTAGTTGTG GCAACCAAGTC CTGACTATGC ACCCTTTGAA TTTCAATCAT TGTTTGATGG	120
AAAGAACCAG GTAGTCGGTG CAGACATCGA CATGGCTCAG GCTATCGCTG ATGAACCTGG	180

GGTTAAGTTG GAAATCTCAA GCATGAGTTT TGACAATGTT TTGACCAGTC TTCAAACTGG 240
 TAAGGCTGAC CTAGCAGTTG CAGGAATTAG TGCTACTGAC GAGAGAAAAG AAGTCTTTGA 300
 TTTTTC AATC CCATACTATG AAAACAAGAT TAGTTTCTTG GTTCGTAAGG CTGATGTGGA 360
 AAAATACAAG GATTTA ACTA GCCTAGAAAAG TGCTAATATT GCAGCCCAA AAGGGACTGT 420
 TCCAGAATCA ATGGTCAAGG AACAAATGCC AAAAGTTCAA TTAAC TTCCC TAACTAATAT 480
 GGGTGAAGCA GTCAATGAAT TGCAGGCTGG AAAAATAGAT GCTGTTTATA TGGATGAGCC 540
 TGTTCACCTT AGTTATGCTG CTAAAAACGC TGGCTTAGCT GTCGCAACTG TCAGCTTGAA 600
 GATGAAGGAC GGCGACGCCA ATGCC 625

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Cys Gln Ser Gly Ser Asn Gly Ser Gln Ser Ala Val Asp Ala Ile Lys
 1 5 10 15
 Gln Lys Gly Lys Leu Val Val Ala Thr Ser Pro Asp Tyr Ala Pro Phe
 20 25 30
 Glu Phe Gln Ser Leu Val Asp Gly Lys Asn Gln Val Val Gly Ala Asp
 35 40 45
 Ile Asp Met Ala Gln Ala Ile Ala Asp Glu Leu Gly Val Lys Leu Glu
 50 55 60
 Ile Ser Ser Met Ser Phe Asp Asn Val Leu Thr Ser Leu Gln Thr Gly
 65 70 75 80
 Lys Ala Asp Leu Ala Val Ala Gly Ile Ser Ala Thr Asp Glu Arg Lys
 85 90 95
 Glu Val Phe Asp Phe Ser Ile Pro Tyr Tyr Glu Asn Lys Ile Ser Phe
 100 105 110
 Leu Val Arg Lys Ala Asp Val Glu Lys Tyr Lys Asp Leu Thr Ser Leu
 115 120 125
 Glu Ser Ala Asn Ile Ala Ala Gln Lys Gly Thr Val Pro Glu Ser Met
 130 135 140
 Val Lys Glu Gln Leu Pro Lys Val Gln Leu Thr Ser Leu Thr Asn Met
 145 150 155 160
 Gly Glu Ala Val Asn Glu Leu Gln Ala Gly Lys Ile Asp Ala Val His

	165		170		175										
Met	Asp	Glu	Pro	Val	Ala	Leu	Ser	Tyr	Ala	Ala	Lys	Asn	Ala	Gly	Leu
	180						185					190			
Ala	Val	Ala	Thr	Val	Ser	Leu	Lys	Met	Lys	Asp	Gly	Asp	Ala	Asn	Ala
	195					200						205			

(2) INFORMATION FOR SEQ ID NO: 215:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3022 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

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GGAAACTTCA CAGGATTTTA AAGAGAAGAA AACAGCAGTC ATTAAGGAAA AAGAAGTTGT	60
TAGTAAAAAT CCTGTGATAG ACAATAACAC TAGCAATGAA GAAGCAAAAA TCAAAGAAGA	120
AAATTCCAAT AAATCCAAG GAGATTATAC GGACTCATTT GTGAATAAAA ACACAGAAAA	180
TCCCAAAAAA GAAGATAAAG TTGTC'TATAT TGCTGAATTT AAAGATAAAG AATCTGGAGA	240
AAAAGCAATC AAGGAAC'TAT CCAGTC'TTAA GAATACAAAA GTTTTATATA CTTATGATAG	300
AATTTTAAAC GGTAGTGCCA TAGAAACAAC TCCAGATAAC TTGGACAAAA TTAAACAAAT	360
AGAAGGTATT TCATCGGTTG AAAGGGCACA AAAAGTCCAA CCCATGATGA ATCATGCCAG	420
AAAGGAAATT GGAGTTGAGG AAGCTATTGA TTACCTAAAG TCTATCAATG CTCCGTTTGG	480
GAAAAATTTT GATGGTAGAG GTATGGTCAT TTCAAATATC GATACTGGAA CAGATTATAG	540
ACATAAGGCT ATGAGAATCG ATGATGATGC CAAAGCCTCA ATGAGATTTA AAAAAGAAGA	600
CTTAAAGGC ACTGATAAAA ATTATTGGTT GAGTGATAAA ATCCCTCATG CGTTCAATTA	660
TTATAATGGT GGCAAAATCA CTGTAGAAAA ATATGATGAT GGAAGGGATT ATTTTGACCC	720
ACATGGGATG CATATTGCAG GGATTCTTGC TGGAAATGAT ACTGAACAAG ACATCAAAAA	780
CTTTAACGGC ATAGATGGAA TTGCACCTAA TGCACAAATT TTCTCTTACA AAATGTATTC	840
TGACGCAGGA TCTGGGTTTG CGGGTGATGA AACAATGTTT CATGCTATTG AAGATTCTAT	900
CAAACACAAC GTTGATGTTG TTTCGGTATC ATCTGGTTTT ACAGGAACAG GTCTTGTAGG	960
TGAGAAATAT TGGCAAGCTA TTCGGGCATT AAGAAAAGCA GGCATTCCAA TGTTTGTCGC	1020
TACGGGTAAC TATGCGACTT CTGCTTCAAG TTCTTCATGG GATTTAGTAG CAAATAATCA	1080
TCTGAAAATG ACCGACACTG GAAATGTAAC ACGAACTGCA GCACATGAAG ATGCGATAGC	1140
GGTCGCTTCT GCTAAAAATC AAACAGTTGA GTTTGATAAA GTTAACATAG GTGGAGAAAG	1200
TTTTAAATAC AGAAATATAG GGGCCTTTTT CGATAAGAGT AAAATCACAA CAAATGAAGA	1260
TGGAACAAAA GCTCCTAGTA AATTAAAATT TGTATATATA GGCAAGGGGC AAGACCAAGA	1320

TTTGATAGGT TTGGATCTTA GGGGCAAAAT TGCAGTAATG GATAGAATTT ATACAAAGGA 1380
 TTTAAAAAAT GCTTTTAAAA AAGCTATGGA TAAGGGTGCA CGGCCCATTA TGGTTGTAAA 1440
 TACTGTAAAT TACTACAATA GAGATAATTG GACAGAGCTT CCAGCTATGG GATATGAAGC 1500
 GGATGAAGGT ACTAAAAGTC AAGTGT'TTTC AAT'TTCAGGA GATGATGGTG TAAAGCTATG 1560
 GAACATGATT AATCCTGATA AAAAACTGA AGTCAAAAGA AATAATAAAG AAGATTTTAA 1620
 AGATAAATG GAGCAATACT ATCCAATTGA TATGGAAAGT TTTAAT'TCCA ACAAACCGAA 1680
 TGTAGGTGAC GAAAAAGAGA TTGACTTTAA GTTTGCACCT GACACAGACA AAGAACTCTA 1740
 TAAAGAAGAT ATCATCGTTC CAGCAGGATC TACATCTTGG GGGCCAAGAA TAGATTTACT 1800
 TTTAAAACCC GATGTTTCAG CACCTGGTAA AAATATTAAA TCCACGCTTA ATGTTATTAA 1860
 TGGCAAATCA ACTTATGGCT ATATGTCAGG AACTAGTATG GCGACTCCAA TCGTGGCAGC 1920
 TTCTACTGTT TTGATTAGAC CGAAATTAAA GGAAATGCTT GAAAGACCTG TATTGAAAAA 1980
 TCTTAAGGGA GATGACAAAA TAGATCTTAC AAGTCTTACA AAAATTGCCC TACAAAATAC 2040
 TGC GCGACCT ATGATGGATG CAACTTCTTG GAAAGAAAAA AGTCAATACT TTGCATCACC 2100
 TAGACAACAG GGAGCAGGCC TAATTAATGT GGCCAATGCT TTGAGAAATG AAGTTGTAGC 2160
 AACTTTTCAA AACACTGATT CTAAAGGTTT GGTAAACTCA TATGGTTCCA TTTCTCTTAA 2220
 AGAAATAAAA GGTGATAAAA AATACTTTAC AATCAAGCTT CACAATACAT CAAACAGACC 2280
 TTTGACTTTT AAAGTTTCAG CATCAGCGAT AACTACAGAT TCTCTAACTG ACAGATTAAA 2340
 ACTTGATGAA ACATATAAAG ATGAAAAATC TCCAGATGGT AAGCAAATTG TTCCAGAAAT 2400
 TCACCCAGAA AAAGTCAAAG GAGCAAATAT CACATTTGAG CATGATACTT TCACTATAGG 2460
 CGCAAATTCT AGCTTTGATT TGAATGCGGT TATAAATGTT GGAGAGGCCA AAAACAAAAA 2520
 TAAATTTGTA GAATCATTTA TTCATTTTGA GTCAGTGGAA GCGATGGAAG CTCTAAACTC 2580
 CAGCGGGAAG AAAATAAACT TCCAACCTTC TTTGTCGATG CCTCTAATGG GATTTGCTGG 2640
 GAATTGGAAC CACGAACCAA TCCTTGATAA ATGGGCTTGG GAAGAAGGGT CAAGATCAAA 2700
 AACACTGGGA GGT'TATGATG ATGATGGTAA ACCGAAAATT CCAGGAACCT TAAATAAGGG 2760
 AATTGGTGGA GAACATGGTA TAGATAAATT TAATCCAGCA GGAGTTATAC AAAATAGAAA 2820
 AGATAAAAAT ACAACATCCC TGGATCAAAA TCCAGAATTA TTTGCTTTCA ATAACGAAGG 2880
 GATCAACGCT CCATCATCAA GTGGTTCTAA GATTGCTAAC ATTTATCCTT TAGATTCAAA 2940
 TGGAAATCCT CAAGATGCTC AACTTGAAAG AGGATTAACA CCTTCTCCAC TTGTATTAAG 3000
 AAGTGCAGAA GAAGGATTGA TT 3022

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1007 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Glu Thr Ser Gln Asp Phe Lys Glu Lys Lys Thr Ala Val Ile Lys Glu
 1 5 10 15
 Lys Glu Val Val Ser Lys Asn Pro Val Ile Asp Asn Asn Thr Ser Asn
 20 25 30
 Glu Glu Ala Lys Ile Lys Glu Glu Asn Ser Asn Lys Ser Gln Gly Asp
 35 40 45
 Tyr Thr Asp Ser Phe Val Asn Lys Asn Thr Glu Asn Pro Lys Lys Glu
 50 55 60
 Asp Lys Val Val Tyr Ile Ala Glu Phe Lys Asp Lys Glu Ser Gly Glu
 65 70 75 80
 Lys Ala Ile Lys Glu Leu Ser Ser Leu Lys Asn Thr Lys Val Leu Tyr
 85 90 95
 Thr Tyr Asp Arg Ile Phe Asn Gly Ser Ala Ile Glu Thr Thr Pro Asp
 100 105 110
 Asn Leu Asp Lys Ile Lys Gln Ile Glu Gly Ile Ser Ser Val Glu Arg
 115 120 125
 Ala Gln Lys Val Gln Pro Met Met Asn His Ala Arg Lys Glu Ile Gly
 130 135 140
 Val Glu Glu Ala Ile Asp Tyr Leu Lys Ser Ile Asn Ala Pro Phe Gly
 145 150 155 160
 Lys Asn Phe Asp Gly Arg Gly Met Val Ile Ser Asn Ile Asp Thr Gly
 165 170 175
 Thr Asp Tyr Arg His Lys Ala Met Arg Ile Asp Asp Asp Ala Lys Ala
 180 185 190
 Ser Met Arg Phe Lys Lys Glu Asp Leu Lys Gly Thr Asp Lys Asn Tyr
 195 200 205
 Trp Leu Ser Asp Lys Ile Pro His Ala Phe Asn Tyr Tyr Asn Gly Gly
 210 215 220
 Lys Ile Thr Val Glu Lys Tyr Asp Asp Gly Arg Asp Tyr Phe Asp Pro
 225 230 235 240
 His Gly Met His Ile Ala Gly Ile Leu Ala Gly Asn Asp Thr Glu Gln
 245 250 255
 Asp Ile Lys Asn Phe Asn Gly Ile Asp Gly Ile Ala Pro Asn Ala Gln
 260 265 270
 Ile Phe Ser Tyr Lys Met Tyr Ser Asp Ala Gly Ser Gly Phe Ala Gly

275	280	285
Asp Glu Thr Met Phe His Ala Ile Glu Asp Ser Ile Lys His Asn Val 290	295	300
Asp Val Val Ser Val Ser Ser Gly Phe Thr Gly Thr Gly Leu Val Gly 305	310	315 320
Glu Lys Tyr Trp Gln Ala Ile Arg Ala Leu Arg Lys Ala Gly Ile Pro 325	330	335
Met Val Val Ala Thr Gly Asn Tyr Ala Thr Ser Ala Ser Ser Ser 340	345	350
Trp Asp Leu Val Ala Asn Asn His Leu Lys Met Thr Asp Thr Gly Asn 355	360	365
Val Thr Arg Thr Ala Ala His Glu Asp Ala Ile Ala Val Ala Ser Ala 370	375	380
Lys Asn Gln Thr Val Glu Phe Asp Lys Val Asn Ile Gly Gly Glu Ser 385	390	395 400
Phe Lys Tyr Arg Asn Ile Gly Ala Phe Phe Asp Lys Ser Lys Ile Thr 405	410	415
Thr Asn Glu Asp Gly Thr Lys Ala Pro Ser Lys Leu Lys Phe Val Tyr 420	425	430
Ile Gly Lys Gly Gln Asp Gln Asp Leu Ile Gly Leu Asp Leu Arg Gly 435	440	445
Lys Ile Ala Val Met Asp Arg Ile Tyr Thr Lys Asp Leu Lys Asn Ala 450	455	460
Phe Lys Lys Ala Met Asp Lys Gly Ala Arg Ala Ile Met Val Val Asn 465	470	475 480
Thr Val Asn Tyr Tyr Asn Arg Asp Asn Trp Thr Glu Leu Pro Ala Met 485	490	495
Gly Tyr Glu Ala Asp Glu Gly Thr Lys Ser Gln Val Phe Ser Ile Ser 500	505	510
Gly Asp Asp Gly Val Lys Leu Trp Asn Met Ile Asn Pro Asp Lys Lys 515	520	525
Thr Glu Val Lys Arg Asn Asn Lys Glu Asp Phe Lys Asp Lys Leu Glu 530	535	540
Gln Tyr Tyr Pro Ile Asp Met Glu Ser Phe Asn Ser Asn Lys Pro Asn 545	550	555 560
Val Gly Asp Glu Lys Glu Ile Asp Phe Lys Phe Ala Pro Asp Thr Asp 565	570	575
Lys Glu Leu Tyr Lys Glu Asp Ile Ile Val Pro Ala Gly Ser Thr Ser 580	585	590
Trp Gly Pro Arg Ile Asp Leu Leu Leu Lys Pro Asp Val Ser Ala Pro 595	600	605
Gly Lys Asn Ile Lys Ser Thr Leu Asn Val Ile Asn Gly Lys Ser Thr		

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cont.

610 615 620
 Tyr Gly Tyr Met Ser Gly Thr Ser Met Ala Thr Pro Ile Val Ala Ala
 625 630 635 640
 Ser Thr Val Leu Ile Arg Pro Lys Leu Lys Glu Met Leu Glu Arg Pro
 645 650 655
 Val Leu Lys Asn Leu Lys Gly Asp Asp Lys Ile Asp Leu Thr Ser Leu
 660 665 670
 Thr Lys Ile Ala Leu Gln Asn Thr Ala Arg Pro Met Met Asp Ala Thr
 675 680 685
 Ser Trp Lys Glu Lys Ser Gln Tyr Phe Ala Ser Pro Arg Gln Gln Gly
 690 695 700
 Ala Gly Leu Ile Asn Val Ala Asn Ala Leu Arg Asn Glu Val Val Ala
 705 710 715 720
 Thr Phe Lys Asn Thr Asp Ser Lys Gly Leu Val Asn Ser Tyr Gly Ser
 725 730 735
 Ile Ser Leu Lys Glu Ile Lys Gly Asp Lys Lys Tyr Phe Thr Ile Lys
 740 745 750
 Leu His Asn Thr Ser Asn Arg Pro Leu Thr Phe Lys Val Ser Ala Ser
 755 760 765
 Ala Ile Thr Thr Asp Ser Leu Thr Asp Arg Leu Lys Leu Asp Glu Thr
 770 775 780
 Tyr Lys Asp Glu Lys Ser Pro Asp Gly Lys Gln Ile Val Pro Glu Ile
 785 790 795 800
 His Pro Glu Lys Val Lys Gly Ala Asn Ile Thr Phe Glu His Asp Thr
 805 810 815
 Phe Thr Ile Gly Ala Asn Ser Ser Phe Asp Leu Asn Ala Val Ile Asn
 820 825 830
 Val Gly Glu Ala Lys Asn Lys Asn Lys Phe Val Glu Ser Phe Ile His
 835 840 845
 Phe Glu Ser Val Glu Ala Met Glu Ala Leu Asn Ser Ser Gly Lys Lys
 850 855 860
 Ile Asn Phe Gln Pro Ser Leu Ser Met Pro Leu Met Gly Phe Ala Gly
 865 870 875 880
 Asn Trp Asn His Glu Pro Ile Leu Asp Lys Trp Ala Trp Glu Glu Gly
 885 890 895
 Ser Arg Ser Lys Thr Leu Gly Gly Tyr Asp Asp Asp Gly Lys Pro Lys
 900 905 910
 Ile Pro Gly Thr Leu Asn Lys Gly Ile Gly Gly Glu His Gly Ile Asp
 915 920 925
 Lys Phe Asn Pro Ala Gly Val Ile Gln Asn Arg Lys Asp Lys Asn Thr
 930 935 940
 Thr Ser Leu Asp Gln Asn Pro Glu Leu Phe Ala Phe Asn Asn Glu Gly

945	950	955	960
Ile Asn Ala Pro Ser Ser Ser Gly Ser Lys Ile Ala Asn Ile Tyr Pro			
965		970	975
Leu Asp Ser Asn Gly Asn Pro Gln Asp Ala Gln Leu Glu Arg Gly Leu			
980	985		990
Thr Pro Ser Pro Leu Val Leu Arg Ser Ala Glu Glu Gly Leu Ile			
995	1000		1005

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

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TGTGGTCGAA GTTGAGACTC CTCAATCAAT AACAAATCAG GAGCAAGCTA GGACAGAAAA	60
CCAAGTAGTA GAGACAGAGG AAGCTCCAAA AGAAGAAGCA CCTAAAACAG AAGAAAGTCC	120
AAAGGAAGAA CCAAAATCGG AGGTAAAACC TACTGACGAC ACCCTTCCTA AAGTAGAAGA	180
GGGGAAAGAA GATTCAGCAG AACCAGCTCC AGTTGAAGAA GTAGGTGGAG AAGTTGAGTC	240
AAAACCAGAG GAAAAAGTAG CAGTTAAGCC AGAAAGTCAA CCATCAGACA AACCAGCTGA	300
GGAATCAAAA GTTGAACAAG CAGGTGAACC AGTCGCGCCA AGAGAAGACG AAAAGGCACC	360
AGTCGAGCCA GAAAAGCAAC CAGAAGCTCC TGAAGAAGAG AAGGCTGTAG AGGAAACACC	420
GAAACAAGAA GAGTCAACTC CAGATACCAA GGCTGAAGAA ACTGTAGAAC CAAAAGAGGA	480
GACTGTTAAT CAATCTATTG AACAACCAA AGTTGAAACG CCTGCTGTAG AAAAACAAC	540
AGAACCAACA GAGGAACCAA AAGTTGAACA AGCAGGTGAA CCAGTCGCGC CAAGAGAAGA	600
CGAACAGGCA CCAACGGCAC CAGTTGAGCC AGAAAAGCAA CCAGAAAGTTC CTGAAGAAGA	660
GAAGGCTGTA GAGGAAACAC CGAAACCAGA AGATAAAATA AAGGGTATTG GTACTAAAGA	720
ACCAGTTGAT AAAAGTGAGT TAAATAATCA AATTGATAAA GCTAGTTCAG TTTCTCCTAC	780
TGATTATTCT ACAGCAAGTT ACAATGCTCT TGGACCTGTT TTAGAACTG CAAAAGGTGT	840
CTATGCTTCA GAGCCTGTAA AACAGCTGA GGTAAATAGC GAGACAAATA AACTTAAAC	900
GGCTATTGAC GCTCTAAACG TTGATAAAAC TGAATTAAAC AATACGATTG CAGATGCAAA	960
AACAAAGGTA AAAGAACATT ACAGTGATAG AAGTTGGCAA AACCTCCAAA CTGAAGTTAC	1020
AAAGGCTGAA AAAGTTGCAG CTAATACAGA TGCTAAACAA AGTGAAGTTA ACGAAGCTGT	1080
TGAAAAATTA ACTGCAACTA TTGAAAAATT GGTGAATTA TCTGAAAAGC CAATATTAAC	1140
ATTGACTAGT ACCGATAAGA AAATATTGGA ACGTGAAGCT GTTGCTAAGT ATACTCTAGA	1200

AAATCAAAAC AAAACAAAA TCAAATCAAT CACAGCTGAA TTGAAAAAG GAGAAGAAGT 1260
TATTAATACT GTAGTCCTTA CAGATGACAA GGTAACAACA GAACTATAA GCGCTGCATT 1320
TAAGAACCTA GAGTACTACA AAGAATACAC CCTATCTACA ACTATGATT ACGACAGAGG 1380
TAACGGTGAA GAACTGAAA CTCTAGAAAA TCAAATATT CAATTAGATC TTAAAAAGT 1440
TGAGCTTAAA AATATTAAAC GTACAGATT AATCAAATAC GAAAATGGAA AAGAACTAA 1500
TGAATCACTG ATAACAATA TTCCTGATGA TAAGAGCAAT TATTATTAA AAATAACTTC 1560
AAATAATCAG AAACTACAT TACTAGCTGT TAAAAATATA GAAGAACTA CGGTTAACGG 1620
AACACCTGTA TATAAGTTA CAGCAATCGC AGACAATTTA GTCTCTAGAA CTGCTGATAA 1680
TAAATTTGAA GAAGAA 1696

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Val Val Glu Val Glu Thr Pro Gln Ser Ile Thr Asn Gln Glu Gln Ala
1 5 10 15
Arg Thr Glu Asn Gln Val Val Glu Thr Glu Glu Ala Pro Lys Glu Glu
20 25 30
Ala Pro Lys Thr Glu Glu Ser Pro Lys Glu Glu Pro Lys Ser Glu Val
35 40 45
Lys Pro Thr Asp Asp Thr Leu Pro Lys Val Glu Glu Gly Lys Glu Asp
50 55 60
Ser Ala Glu Pro Ala Pro Val Glu Glu Val Gly Gly Glu Val Glu Ser
65 70 75 80
Lys Pro Glu Glu Lys Val Ala Val Lys Pro Glu Ser Gln Pro Ser Asp
85 90 95
Lys Pro Ala Glu Glu Ser Lys Val Glu Gln Ala Gly Glu Pro Val Ala
100 105 110
Pro Arg Glu Asp Glu Lys Ala Pro Val Glu Pro Glu Lys Gln Pro Glu
115 120 125
Ala Pro Glu Glu Glu Lys Ala Val Glu Glu Thr Pro Lys Gln Glu Glu
130 135 140
Ser Thr Pro Asp Thr Lys Ala Glu Glu Thr Val Glu Pro Lys Glu Glu
145 150 155 160

Thr Val Asn Gln Ser Ile Glu Gln Pro Lys Val Glu Thr Pro Ala Val
 165 170 175
 Glu Lys Gln Thr Glu Pro Thr Glu Glu Pro Lys Val Glu Gln Ala Gly
 180 185 190
 Glu Pro Val Ala Pro Arg Glu Asp Glu Gln Ala Pro Thr Ala Pro Val
 195 200 205
 Glu Pro Glu Lys Gln Pro Glu Val Pro Glu Glu Glu Lys Ala Val Glu
 210 215 220
 Glu Thr Pro Lys Pro Glu Asp Lys Ile Lys Gly Ile Gly Thr Lys Glu
 225 230 235 240
 Pro Val Asp Lys Ser Glu Leu Asn Asn Gln Ile Asp Lys Ala Ser Ser
 245 250 255
 Val Ser Pro Thr Asp Tyr Ser Thr Ala Ser Tyr Asn Ala Leu Gly Pro
 260 265 270
 Val Leu Glu Thr Ala Lys Gly Val Tyr Ala Ser Glu Pro Val Lys Gln
 275 280 285
 Pro Glu Val Asn Ser Glu Thr Asn Lys Leu Lys Thr Ala Ile Asp Ala
 290 295 300
 Leu Asn Val Asp Lys Thr Glu Leu Asn Asn Thr Ile Ala Asp Ala Lys
 305 310 315 320
 Thr Lys Val Lys Glu His Tyr Ser Asp Arg Ser Trp Gln Asn Leu Gln
 325 330 335
 Thr Glu Val Thr Lys Ala Glu Lys Val Ala Ala Asn Thr Asp Ala Lys
 340 345 350
 Gln Ser Glu Val Asn Glu Ala Val Glu Lys Leu Thr Ala Thr Ile Glu
 355 360 365
 Lys Leu Val Glu Leu Ser Glu Lys Pro Ile Leu Thr Leu Thr Ser Thr
 370 375 380
 Asp Lys Lys Ile Leu Glu Arg Glu Ala Val Ala Lys Tyr Thr Leu Glu
 385 390 395 400
 Asn Gln Asn Lys Thr Lys Ile Lys Ser Ile Thr Ala Glu Leu Lys Lys
 405 410 415
 Gly Glu Glu Val Ile Asn Thr Val Val Leu Thr Asp Asp Lys Val Thr
 420 425 430
 Thr Glu Thr Ile Ser Ala Ala Phe Lys Asn Leu Glu Tyr Tyr Lys Glu
 435 440 445
 Tyr Thr Leu Ser Thr Thr Met Ile Tyr Asp Arg Gly Asn Gly Glu Glu
 450 455 460
 Thr Glu Thr Leu Glu Asn Gln Asn Ile Gln Leu Asp Leu Lys Lys Val
 465 470 475 480
 Glu Leu Lys Asn Ile Lys Arg Thr Asp Leu Ile Lys Tyr Glu Asn Gly
 485 490 495

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Lys Glu Thr Asn Glu Ser Leu Ile Thr Thr Ile Pro Asp Asp Lys Ser
 500 505 510
 Asn Tyr Tyr Leu Lys Ile Thr Ser Asn Asn Gln Lys Thr Thr Leu Leu
 515 520 525
 Ala Val Lys Asn Ile Glu Glu Thr Thr Val Asn Gly Thr Pro Val Tyr
 530 535 540
 Lys Val Thr Ala Ile Ala Asp Asn Leu Val Ser Arg Thr Ala Asp Asn
 545 550 555 560
 Lys Phe Glu Glu Glu
 565

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

AACACCTGTA TATAAAGTTA CAGCAATCGC AGACAATTTA GTCTCTAGAA CTGCTGATAA 60
 TAAATTTGAA GAAGAATACG TTCACTATAT TGAAAAACCT AAAGTCCACG AAGATAATGT 120
 ATATTATAAT TTCAAAGAAT TAGTGGAAGC TATTCAAAAC GATCCTTCAA AAGAATATCG 180
 TCTGGGACAA TCAATGAGCG CTAGAAATGT TGTTCCTAAT GGAAAATCAT ATATCACTAA 240
 AGAATTCACA GGAAACTTTT TAAGTTCTGA AGGAAAACAA TTTGCTATTA CTGAATTGGA 300
 ACATCCATTA TTTAATGTGA TAACAAACGC AACGATAAAT AATGTGAATT TTGAAAATGT 360
 AGAGATAGAA CGTTCTGGTC AAGATAATAT TGCATCATTG GCCAATACTA TGAAAGGTTC 420
 TTCAGTTATT ACAAATGTCA AAATTACAGG CACACTTTCA GGTCGTAATA ATGTTGCTGG 480
 ATTTGTAAAT AATATGAATG ATGGAACTCG TATTGAAAAT GTTGCTTTCT TTGGCAAAC 540
 ACACTCTACA AGTGGAAATG GCTCTCATAC AGGGGGAATT GCAGGTACAA ACTATAGAGG 600
 AATTGTTAGA AAAGCATATG TTGATGCTAC TATTACAGGA AACAAAACAC GCGCCAGCTT 660
 GTTAGTTCCT AAAGTAGAAT ATGGATTAACT TCTAGACCAT CTTATTGGTA CAAAAGCTCT 720
 CCTAAGTGA TCGGTTGTAA AAGGTAAAAT AGATGTTTCA AATCCAGTAG AAGTTGGAGC 780
 AATAGCAAGT AAGACTTGGC CTGTAGGTAC GGTAAGTAAT TCTGTCAGCT ATGCTAAGAT 840
 TATCCGTGGA GAGGAGTTAT TCGGCTCTAA CGACGTTGAT GATTCTGATT ATGCTAGTGC 900
 TCATATAAAA GATTTATATG CGGTAGAGGG ATATTCTGTA GGTAATAGAT CATTTAGGAA 960
 ATCTAAAAACA TTACTAAAT TAACTAAAGA ACAAGCTGAT GCTAAAGTTA CTAATTTCAA 1020
 TATTACTGCT GATAAATTAG AAAGTGATCT ATCTCCTCTT GCAAACTTA ATGAAGAAAA 1080

AGCCTATTCT AGTATTCAAG ATTATAACGC TGAATATAAC CAAGCCTATA AAAATCTTGA 1140
 AAAATTAATA CCATTCTACA ATAAAGATTA TATTGTATAT CAAGGTAATA AATTAAATAA 1200
 AGAACACCAT CTAAATACTA AAGAAGTTCT TTCTGTTACC GCGATGAACA ACAATGAGTT 1260
 TATCACAAAC CTAGATGAAG CTAATAAAAT TATTGTTTAC TATGCGGACG GTACAAAAGA 1320
 TTACTTTAAC TTGTCTTCTA GCAGTGAAGG TTTAAGTAAT GTAAAAGAAT ATACTATAAC 1380
 TGACTTAGGA ATTAAATATA CACCTAATAT CGTTCAAAAA GATAACACTA CTCTTGTTAA 1440
 TGATATAAAA TCTATTTTAG AATCAGTAGA GCTTCAGTCT CAAACGATGT ATCAGCATCT 1500
 AAATCGATTA GGTGACTATA GAGTTAATGC AATCAAAGAT TTATATTTAG AAGAAAGCTT 1560
 CACAGATGTT AAAGAAAAC TAACAAACCT AATCACAAAA TTAGTTCAAA ACGAAGAACA 1620
 TCAACTAAAT GATTCTCCAG CTGCTCGTCA AATGATTCGT GATAAAGTCG AGAAAAACAA 1680
 AGCAGCTTTA TTACTAGGTT TAACTTACCT AAATCGTTAC TATGGAGTTA AATTTGGTGA 1740
 TGTTAATATT AAAGAATTAA TGCTATTCAA ACCAGATTTC TATGGTGAAA AAGTTAGCGT 1800
 ATTAGACAGA TTAATTGAAA TCGGTTCTAA AGAGAACAAC ATTAAAGGTT CACGTACATT 1860
 CGACGCATTC GGTCAAGTA 1879

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Thr Pro Val Tyr Lys Val Thr Ala Ile Ala Asp Asn Leu Val Ser Arg
 1 5 10 15
 Thr Ala Asp Asn Lys Phe Glu Glu Glu Tyr Val His Tyr Ile Glu Lys
 20 25 30
 Pro Lys Val His Glu Asp Asn Val Tyr Tyr Asn Phe Lys Glu Leu Val
 35 40 45
 Glu Ala Ile Gln Asn Asp Pro Ser Lys Glu Tyr Arg Leu Gly Gln Ser
 50 55 60
 Met Ser Ala Arg Asn Val Val Pro Asn Gly Lys Ser Tyr Ile Thr Lys
 65 70 75 80
 Glu Phe Thr Gly Lys Leu Leu Ser Ser Glu Gly Lys Gln Phe Ala Ile
 85 90 95
 Thr Glu Leu Glu His Pro Leu Phe Asn Val Ile Thr Asn Ala Thr Ile
 100 105 110

Asn Asn Val Asn Phe Glu Asn Val Glu Ile Glu Arg Ser Gly Gln Asp
 115 120 125
 Asn Ile Ala Ser Leu Ala Asn Thr Met Lys Gly Ser Ser Val Ile Thr
 130 135 140
 Asn Val Lys Ile Thr Gly Thr Leu Ser Gly Arg Asn Asn Val Ala Gly
 145 150 155 160
 Phe Val Asn Asn Met Asn Asp Gly Thr Arg Ile Glu Asn Val Ala Phe
 165 170 175
 Phe Gly Lys Leu His Ser Thr Ser Gly Asn Gly Ser His Thr Gly Gly
 180 185 190
 Ile Ala Gly Thr Asn Tyr Arg Gly Ile Val Arg Lys Ala Tyr Val Asp
 195 200 205
 Ala Thr Ile Thr Gly Asn Lys Thr Arg Ala Ser Leu Leu Val Pro Lys
 210 215 220
 Val Asp Tyr Gly Leu Thr Leu Asp His Leu Ile Gly Thr Lys Ala Leu
 225 230 235 240
 Leu Thr Glu Ser Val Val Lys Gly Lys Ile Asp Val Ser Asn Pro Val
 245 250 255
 Glu Val Gly Ala Ile Ala Ser Lys Thr Trp Pro Val Gly Thr Val Ser
 260 265 270
 Asn Ser Val Ser Tyr Ala Lys Ile Ile Arg Gly Glu Glu Leu Phe Gly
 275 280 285
 Ser Asn Asp Val Asp Asp Ser Asp Tyr Ala Ser Ala His Ile Lys Asp
 290 295 300
 Leu Tyr Ala Val Glu Gly Tyr Ser Ser Gly Asn Arg Ser Phe Arg Lys
 305 310 315 320
 Ser Lys Thr Phe Thr Lys Leu Thr Lys Glu Gln Ala Asp Ala Lys Val
 325 330 335
 Thr Thr Phe Asn Ile Thr Ala Asp Lys Leu Glu Ser Asp Leu Ser Pro
 340 345 350
 Leu Ala Lys Leu Asn Glu Glu Lys Ala Tyr Ser Ser Ile Gln Asp Tyr
 355 360 365
 Asn Ala Glu Tyr Asn Gln Ala Tyr Lys Asn Leu Glu Lys Leu Ile Pro
 370 375 380
 Phe Tyr Asn Lys Asp Tyr Ile Val Tyr Gln Gly Asn Lys Leu Asn Lys
 385 390 395 400
 Glu His His Leu Asn Thr Lys Glu Val Leu Ser Val Thr Ala Met Asn
 405 410 415
 Asn Asn Glu Phe Ile Thr Asn Leu Asp Glu Ala Asn Lys Ile Ile Val
 420 425 430
 His Tyr Ala Asp Gly Thr Lys Asp Tyr Phe Asn Leu Ser Ser Ser Ser
 435 440 445

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Glu Gly Leu Ser Asn Val Lys Glu Tyr Thr Ile Thr Asp Leu Gly Ile
 450 455 460
 Lys Tyr Thr Pro Asn Ile Val Gln Lys Asp Asn Thr Thr Leu Val Asn
 465 470 475 480
 Asp Ile Lys Ser Ile Leu Glu Ser Val Glu Leu Gln Ser Gln Thr Met
 485 490 495
 Tyr Gln His Leu Asn Arg Leu Gly Asp Tyr Arg Val Asn Ala Ile Lys
 500 505 510
 Asp Leu Tyr Leu Glu Glu Ser Phe Thr Asp Val Lys Glu Asn Leu Thr
 515 520 525
 Asn Leu Ile Thr Lys Leu Val Gln Asn Glu Glu His Gln Leu Asn Asp
 530 535 540
 Ser Pro Ala Ala Arg Gln Met Ile Arg Asp Lys Val Glu Lys Asn Lys
 545 550 555 560
 Ala Ala Leu Leu Leu Gly Leu Thr Tyr Leu Asn Arg Tyr Tyr Gly Val
 565 570 575
 Lys Phe Gly Asp Val Asn Ile Lys Glu Leu Met Leu Phe Lys Pro Asp
 580 585 590
 Phe Tyr Gly Glu Lys Val Ser Val Leu Asp Arg Leu Ile Glu Ile Gly
 595 600 605
 Ser Lys Glu Asn Asn Ile Lys Gly Ser Arg Thr Phe Asp Ala Phe Gly
 610 615 620
 Gln Val
 625

(2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

ATTAGACAGA TTAATTGAAA TCGGTTCTAA AGAGAACAAC ATTAAAGGTT CACGTACATT	60
CGACGCATTC GGTCAAGTAT TGGCTAAATA TACTAAATCA GGTAATTTAG ATGCATTTMT	120
AAATTATAAT AGACAATTGT TCACAAATAT AGACAATATG AACGATTGGT TTATTGATGC	180
TACAGAAGAC CATGTCTACA TCGCAGAACG CGCTTCTGAG GTCGAAGAAA TTAAAAATTC	240
TAAACATCGT GCATTCGATA ATTTAAAACG AAGTCACCTT AGAAATACTA TACTCCCACT	300
ACTGAATATT GATAAAGCAC ATCTTTATTT AATTTCAAAT TATAATGCAA TTGCCTTTGG	360
TAGTGCAGAG CGATTAGGTA AAAAATCATT AGAAGATATT AAAGATATCG TTAACAAAGC	420

TGCAGATGGT TATAGAACT ATTATGATT CTGGTATCGT CTAGCGTCTG ATAACGTTAA 480
 ACAACGACTA CTAAGAGATG CTGTTATTCC TATTTGGGAA GGTTATAACG CTCCTGGTGG 540
 ATGGGTTGAA AAATATGGCC GCTATAATAC CGACAAAGTA TATACTCCTC TTAGAGAATT 600
 CTTTGGTCCT ATGGATAAGT ATTATAATTA TAATGGAACA GGAGCTTATG CTGCTATATA 660
 TCCTAACTCT GATGATATTA GAACTGATGT AAAATATGTT CATTTAGAAA TGGTTGGTGA 720
 ATACGGTATT TCAGTTTACA CACATGAAAC AACACACGTC AACGACCGTG CGATTTACTT 780
 AGGTGGCTTT GGACACCGTG AAGGTACTGA TGCTGAAGCA TATGCTCAGG GTATGCTACA 840
 AACTCCTGTT ACTGGTAGTG GATTTGATGA GTTTGGTTCT TTAGGTATTA ATATGGTATT 900
 TAAACGCAAA AATGATGGGA ATCAGTGGTA TATTACAGAT CCAAAAACCTC TAAAAACACG 960
 AGAAGATATT AATAGATATA TGAAGGGTTA TAATGACACT TTAACCTCTC TTGATGAAAT 1020
 TGAGGCTGAA TCTGTGATTT CTCAACAAAA TAAAGATTTA AATAGTGCAT GGTTCAAAAA 1080
 AATAGATAGA GAATACCGTG ATAACAATAA ATTAAATCAA TGGGATAAAA TTCGAAATCT 1140
 AAGTCAAGAA GAGAAAAATG AATTAAATAT TCAATCTGTT AATGATTTAG TTGATCAACA 1200
 ATTAATGACT AATCGCAATC CAGGTAATGG TATCTATAAA CCCGAAGCAA TTAGCTATAA 1260
 CGATCAATCA CCTTATGTAG GTGTTAGAAT GATGACCGGT ATCTACGGAG GTAATACTAG 1320
 TAAAGGTGCT CCTGGAGCTG TTTCAITCAA ACATAATGCT TTTAGATTAT GGGGTTACTA 1380
 CGGATACGAA AATGGGTTCT TAGGTTATGC TTCAAATAAA TATAACAAC AATCTAAAAC 1440
 AGATGGTGAG TCTGTTCTAA GTGATGAATA TATTATCAAG AAAATATCTA ACAATACATT 1500
 TAATACTATT GAAGAATTTA AAAAAGCTTA CTTCAAAGAA GTTAAAGATA AAGCAACGAA 1560
 AGGATTAACA ACATTGGAAG TAAATGGTTC TTCCGTTTCA TCATACGATG ATTTACTGAC 1620
 ATTGTTTTAA GAAGCTGTTA AAAAAGATGC CGAAACTCTT AAACAAGAAG CAAACGGTAA 1680
 TAAAACAGTA TCTATGAATA ATACAGTTAA ATTAAAAGAA GCTGTTTATA AGAACTTCT 1740
 TCAACAAACA AATAGCTTTA AACTTCAAT CTTTAAA 1777

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 592 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Leu Asp Arg Leu Ile Glu Ile Gly Ser Lys Glu Asn Asn Ile Lys Gly
 1 5 10 15

Ser Arg Thr Phe Asp Ala Phe Gly Gln Val Leu Ala Lys Tyr Thr Lys
 20 25 30
 Ser Gly Asn Leu Asp Ala Phe Leu Asn Tyr Asn Arg Gln Leu Phe Thr
 35 40 45
 Asn Ile Asp Asn Met Asn Asp Trp Phe Ile Asp Ala Thr Glu Asp His
 50 55 60
 Val Tyr Ile Ala Glu Arg Ala Ser Glu Val Glu Glu Ile Lys Asn Ser
 65 70 75 80
 Lys His Arg Ala Phe Asp Asn Leu Lys Arg Ser His Leu Arg Asn Thr
 85 90 95
 Ile Leu Pro Leu Leu Asn Ile Asp Lys Ala His Leu Tyr Leu Ile Ser
 100 105 110
 Asn Tyr Asn Ala Ile Ala Phe Gly Ser Ala Glu Arg Leu Gly Lys Lys
 115 120 125
 Ser Leu Glu Asp Ile Lys Asp Ile Val Asn Lys Ala Ala Asp Gly Tyr
 130 135 140
 Arg Asn Tyr Tyr Asp Phe Trp Tyr Arg Leu Ala Ser Asp Asn Val Lys
 145 150 155 160
 Gln Arg Leu Leu Arg Asp Ala Val Ile Pro Ile Trp Glu Gly Tyr Asn
 165 170 175
 Ala Pro Gly Gly Trp Val Glu Lys Tyr Gly Arg Tyr Asn Thr Asp Lys
 180 185 190
 Val Tyr Thr Pro Leu Arg Glu Phe Phe Gly Pro Met Asp Lys Tyr Tyr
 195 200 205
 Asn Tyr Asn Gly Thr Gly Ala Tyr Ala Ala Ile Tyr Pro Asn Ser Asp
 210 215 220
 Asp Ile Arg Thr Asp Val Lys Tyr Val His Leu Glu Met Val Gly Glu
 225 230 235 240
 Tyr Gly Ile Ser Val Tyr Thr His Glu Thr Thr His Val Asn Asp Arg
 245 250 255
 Ala Ile Tyr Leu Gly Gly Phe Gly His Arg Glu Gly Thr Asp Ala Glu
 260 265 270
 Ala Tyr Ala Gln Gly Met Leu Gln Thr Pro Val Thr Gly Ser Gly Phe
 275 280 285
 Asp Glu Phe Gly Ser Leu Gly Ile Asn Met Val Phe Lys Arg Lys Asn
 290 295 300
 Asp Gly Asn Gln Trp Tyr Ile Thr Asp Pro Lys Thr Leu Lys Thr Arg
 305 310 315 320
 Glu Asp Ile Asn Arg Tyr Met Lys Gly Tyr Asn Asp Thr Leu Thr Leu
 325 330 335
 Leu Asp Glu Ile Glu Ala Glu Ser Val Ile Ser Gln Gln Asn Lys Asp
 340 345 350

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 cont.

Leu Asn Ser Ala Trp Phe Lys Lys Ile Asp Arg Glu Tyr Arg Asp Asn
 355 360 365
 Asn Lys Leu Asn Gln Trp Asp Lys Ile Arg Asn Leu Ser Gln Glu Glu
 370 375 380
 Lys Asn Glu Leu Asn Ile Gln Ser Val Asn Asp Leu Val Asp Gln Gln
 385 390 395 400
 Leu Met Thr Asn Arg Asn Pro Gly Asn Gly Ile Tyr Lys Pro Glu Ala
 405 410 415
 Ile Ser Tyr Asn Asp Gln Ser Pro Tyr Val Gly Val Arg Met Met Thr
 420 425 430
 Gly Ile Tyr Gly Gly Asn Thr Ser Lys Gly Ala Pro Gly Ala Val Ser
 435 440 445
 Phe Lys His Asn Ala Phe Arg Leu Trp Gly Tyr Tyr Gly Tyr Glu Asn
 450 455 460
 Gly Phe Leu Gly Tyr Ala Ser Asn Lys Tyr Lys Gln Gln Ser Lys Thr
 465 470 475 480
 Asp Gly Glu Ser Val Leu Ser Asp Glu Tyr Ile Ile Lys Lys Ile Ser
 485 490 495
 Asn Asn Thr Phe Asn Thr Ile Glu Glu Phe Lys Lys Ala Tyr Phe Lys
 500 505 510
 Glu Val Lys Asp Lys Ala Thr Lys Gly Leu Thr Thr Phe Glu Val Asn
 515 520 525
 Gly Ser Ser Val Ser Ser Tyr Asp Asp Leu Leu Thr Leu Phe Lys Glu
 530 535 540
 Ala Val Lys Lys Asp Ala Glu Thr Leu Lys Gln Glu Ala Asn Gly Asn
 545 550 555 560
 Lys Thr Val Ser Met Asn Asn Thr Val Lys Leu Lys Glu Ala Val Tyr
 565 570 575
 Lys Lys Leu Leu Gln Gln Thr Asn Ser Phe Lys Thr Ser Ile Phe Lys
 580 585 590

(2) INFORMATION FOR SEQ ID NO: 223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 460 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

TAAGACAGAT GAACGGAGCA AGGTGTTTGA CTTTTCATT CCCTACTATA CTGCAAAAAA	60
TAAACTCATT GTCAAAAAAT CTGACTTGAC TACTTATCAG TCTGTAAACG ACTTGCGCA	120
GAAAAAGGTT GGAGCGCAGA AAGGTTTCGAT TCAAGAGACG ATGGCGAAAG ATTTGCTACA	180

AAATCTTCC CTCGTATCTC TGCCTAAAAA TGGGAATTTA ATCACAGATT TAAAATCAGG 240
 ACAAGTGGAT GCCGTATCTT TTGAAGAACC TGTTTCCAAG GGATTTGTGG AAAATAATCC 300
 TGATTTAGCA ATCGCAGACC TCAATTTTGA AAAAGAGCAA GATGATTCCT ACGCGGTAGC 360
 CATgAAAAAA GATAGCAAGA AATTGAAGAG GCAGTTCGAT AAAACCATTC AAAAGTTGAA 420
 GGAGTCTGGG GAATTAGACA AACTCATTGA GGAAGCCTTA 460

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Lys Thr Asp Glu Arg Ser Lys Val Phe Asp Phe Ser Ile Pro Tyr Tyr
 1 5 10 15
 Thr Ala Lys Asn Lys Leu Ile Val Lys Lys Ser Asp Leu Thr Thr Tyr
 20 25 30
 Gln Ser Val Asn Asp Leu Ala Gln Lys Lys Val Gly Ala Gln Lys Gly
 35 40 45
 Ser Ile Gln Glu Thr Met Ala Lys Asp Leu Leu Gln Asn Ser Ser Leu
 50 55 60
 Val Ser Leu Pro Lys Asn Gly Asn Leu Ile Thr Asp Leu Lys Ser Gly
 65 70 75 80
 Gln Val Asp Ala Val Ile Phe Glu Glu Pro Val Ser Lys Gly Phe Val
 85 90 95
 Glu Asn Asn Pro Asp Leu Ala Ile Ala Asp Leu Asn Phe Glu Lys Glu
 100 105 110
 Gln Asp Asp Ser Tyr Ala Val Ala Met Lys Lys Asp Ser Lys Lys Leu
 115 120 125
 Lys Arg Gln Phe Asp Lys Thr Ile Gln Lys Leu Lys Glu Ser Gly Glu
 130 135 140
 Leu Asp Lys Leu Ile Glu Glu Ala Leu
 145 150

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

CTGTGAGAAT CAAGCTACAC CCAAAGAGAC TAGCGCTCAA AAGACAATCG TCCTTGCTAC 60
 AGCTGGCGAC GTGCCACCAT TTGACTACGA AGACAAGGGC AATCTGACAG GCTTTGATAT 120
 CGAAGTTTTA AAGGCAGTAG ATGAAAAACT CAGCGACTAC GAGATTCAAT TCCAAAGAAC 180
 CGCCTGGGAG AGCATCTTCC CAGGACTTGA TTCTGGTCAC TATCAGGCTG CGGCCAATAA 240
 CTTGAGTTAC ACAAAGAGC GTGCTGAAAA ATACCTTTAC TCGCTTCCAA TTTCCAACAA 300
 TCCCCTCGTC CTTGTGAGCA ACAAGAAAAA TCCTTTGACT TCTCTTGACC AGATCGCTGG 360
 TAAAACAACA CAAGAGGATA CCGGAAC TTC TACGCTCAA TTCATCAATA ACTGGAATCA 420
 GAAACACACT GATAATCCCG CTACAATTAA TTTTCTGGT GAGGATATG GTAAACGAAT 480
 CCTAGACCTT GCTAACGGAG AGTTTGATT CTAGTTT GACAAGGTAT CCGTTCAAAA 540
 GATTATCAAG GACCGTGGTT TAGACCTCTC AGTCGTTGAT TTACCTTCTG CAGATAGCCC 600
 CAGCAATTAT ATCATTTTCT CAAGCGACCA AAAAGAGTTT AAAGAGCAAT TTGATAAAGC 660
 GCTCAAAGAA CTCTATCAAG ACGGAACCCT TGAAAACTC AGCAATACCT ATCTAGGTGG 720
 TTCTTACCTC CCAGATCAAT CTCAGTTACA A 751

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Cys Glu Asn Gln Ala Thr Pro Lys Glu Thr Ser Ala Gln Lys Thr Ile
 1 5 10 15
 Val Leu Ala Thr Ala Gly Asp Val Pro Pro Phe Asp Tyr Glu Asp Lys
 20 25 30
 Gly Asn Leu Thr Gly Phe Asp Ile Glu Val Leu Lys Ala Val Asp Glu
 35 40 45
 Lys Leu Ser Asp Tyr Glu Ile Gln Phe Gln Arg Thr Ala Trp Glu Ser
 50 55 60
 Ile Phe Pro Gly Leu Asp Ser Gly His Tyr Gln Ala Ala Ala Asn Asn
 65 70 75 80
 Leu Ser Tyr Thr Lys Glu Arg Ala Glu Lys Tyr Leu Tyr Ser Leu Pro
 85 90 95

Ile Ser Asn Asn Pro Leu Val Leu Val Ser Asn Lys Lys Asn Pro Leu
100 105 110

Thr Ser Leu Asp Gln Ile Ala Gly Lys Thr Thr Gln Glu Asp Thr Gly
115 120 125

Thr Ser Asn Ala Gln Phe Ile Asn Asn Trp Asn Gln Lys His Thr Asp
130 135 140

Asn Pro Ala Thr Ile Asn Phe Ser Gly Glu Asp Ile Gly Lys Arg Ile
145 150 155 160

Leu Asp Leu Ala Asn Gly Glu Phe Asp Phe Leu Val Phe Asp Lys Val
165 170 175

Ser Val Gln Lys Ile Ile Lys Asp Arg Gly Leu Asp Leu Ser Val Val
180 185 190

Asp Leu Pro Ser Ala Asp Ser Pro Ser Asn Tyr Ile Ile Phe Ser Ser
195 200 205

Asp Gln Lys Glu Phe Lys Glu Gln Phe Asp Lys Ala Leu Lys Glu Leu
210 215 220

Tyr Gln Asp Gly Thr Leu Glu Lys Leu Ser Asn Thr Tyr Leu Gly Gly
225 230 235 240

Ser Tyr Leu Pro Asp Gln Ser Gln Leu Gln
245 250

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 (2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

GACTGGATCC TAAATCTAC GACAATAAAA ATC

33

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

CTGAGTCGAC TGGTTGTGCT GGTGAG

27

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

GTCAGGATCC AAATTACAAT ACGGACTATG

30

(2) INFORMATION FOR SEQ ID NO: 230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CAGTGTGCGAC TAACTCTAGG TCGGAAAC

28

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

GACTGGATCC TGAGAATCAA GCTACACCCA AAGAG

35

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

AGTCAAGCTT TTGTAACTGA GATTGATCTG G

31

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GACTGGATCC TGGTAACCGC TCTTCTCGTA ACGCAGC

37

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

AGTCAAGCTT TTTCAGGAAC TTTTACGCTT CC

32

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

AGTCAGATCT TGTGAAATT TGACAGGTAA CAGCAAAAAA GCTGC

45

(2) INFORMATION FOR SEQ ID NO: 236:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

ACTGAAGCTT TTTTGTTTTT CAAGAATTCA TCG

33

(2) INFORMATION FOR SEQ ID NO: 237:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

GACTGGATCC TGGTCAAGGA ACTGCTTCTA AAGAC

35

(2) INFORMATION FOR SEQ ID NO: 238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

AGTCAAGCTT TCACAAATTC GTTGGTGAAG CC

32

(2) INFORMATION FOR SEQ ID NO: 239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

GACTGGATCC TAGCTCAGGT GGAAACGCTG GTTCATCC

38

(2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

AGTCAAGCTT ATCAACTTTT CCACCTTCAA CAACC

35

(2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

GTCAAGATCT CTCCAATAT GGTAATCTG CGGATGG

37

(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

AGTCCTGCAG ATCCACATCC GCTTTCATCG GGTAAAGAA GG

42

(2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

GACTGGATCC TGGGAAAAAT TCTAGCGAAA CTAGTGG

37

(2) INFORMATION FOR SEQ ID NO: 244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

GTCACCTGCAG CTGTCCTTCT TTTACTTCTT TGGTTGC

37

(2) INFORMATION FOR SEQ ID NO: 245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

GACTGGATCC TGCTAGCGGA AAAAAAGATA CAACTTCTGG

40

(2) INFORMATION FOR SEQ ID NO: 246:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

CTGAAAGCTT TTTTGCCAAT CCTTCAGCAA TCTTGTC

37

(2) INFORMATION FOR SEQ ID NO: 247:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

GACTAGATCT TGGCTCAAAA AATACAGCTT CAAGTCC

37

(2) INFORMATION FOR SEQ ID NO: 248:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

AGTCCTGCAG GTTTTGTGTT GCTTGGTATT GGTCG

35

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

GACTGGATCC TAGTACAAAC TCAAGCACTA GTCAGACAGA G

41

(2) INFORMATION FOR SEQ ID NO: 250:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

CAGTCTGCAG TTTCAAAGCT TTTTGTATGT CTTC

34

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

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GACTGGATCC TGGCAATTCT GCGGAAGTA AAGATGC

37

(2) INFORMATION FOR SEQ ID NO: 252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

AGTCAAGCTT GTTTCATAGC TTTTGTGATT GTTTCG

36

(2) INFORMATION FOR SEQ ID NO: 253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

GACTGGATCC TTCACAAGAA AAAACAAAAA ATGAAGATGG

40

(2) INFORMATION FOR SEQ ID NO: 254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

AGTCAAGCTT ATCGACGTAG TCTCCGCCTT C

31

(2) INFORMATION FOR SEQ ID NO: 255:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

GACTGGATCC GAAAGGTCTG TGGTCAAATA ATCTTACC

38

(2) INFORMATION FOR SEQ ID NO: 256:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

AGTCAAGCTT AGAGTTAACA TGGTGCTTGC CAATAGG

37

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

GACTGGATCC AAATCAGAA AAGAAAGCAG ACAATGC

37

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

AGTCAAGCTT CCAAAGTGGT TGATCCAAAC CATCTG

36

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

GACTGGATCC TTCGAAAGGG TCAGAAGGTG CAGACC

36

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

AGTCAAGCTT CTGTAGGCTT GGTGTGCCCC AGTTGC

36

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

CTGAGGATCC GGGGATGGCA GCTTTTAAAA ATC

33

(2) INFORMATION FOR SEQ ID NO: 262:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

CAGTAAGCTT GTTTACCCAT TCACCATTAC C

31

(2) INFORMATION FOR SEQ ID NO: 263:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CAGTGGATCC AGACGAGCAA AAAATTAAG

29

(2) INFORMATION FOR SEQ ID NO: 264:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

TCAGAAGCTT GTTTACCCAT TCACCATT

28

(2) INFORMATION FOR SEQ ID NO: 265:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

GACTGGATCC CTGTGGTGAG GAAGAACTA AAAAG

35

(2) INFORMATION FOR SEQ ID NO: 266:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

CTGAGTCGAC AATATTCTGT AGGAATGCTT CGAATTGT

38

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

CTGAGGATCC GACTTTTAAC AATAAACTA TTGAAGAG

38

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

GTCACGTCAG GTTGTCACCT CCAAAAATCA CGG

33

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

GACTGGATCC CTTTACAGGT AAACAACACTAC AAGTCGG

37

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

CAGTAAGCTT TTCGAAGTTT GGCTCAGAAT TG

32

(2) INFORMATION FOR SEQ ID NO: 271:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

GACTGGATCC CCAGGCTGAT ACAAGTATCG CA

32

(2) INFORMATION FOR SEQ ID NO: 272:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

CAGTAAGCTT ATCTGCAGTA TGGCTAGATG G

31

(2) INFORMATION FOR SEQ ID NO: 273:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

GACTGGATCC GTCTGTATCA TTTGAAAACA AAGAAAC

37

(2) INFORMATION FOR SEQ ID NO: 274:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

CAGTCTGCAG TTTTACTGTT GCTGTGCTTG TG

32

(2) INFORMATION FOR SEQ ID NO: 275:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

ACTGAGATCT TGGTCAAAAG GAAAGTCAGA CAGGAAAGG

39

(2) INFORMATION FOR SEQ ID NO: 276:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CAGTAAGCTT ATTCCTGAGC TTTTGTGATA AAGGTTGCGC A

41

(2) INFORMATION FOR SEQ ID NO: 277:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

ACTGGGATCC GAAGGATAGA TATATTTTAG CATTTGAGAC

40

(2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

AGTCAAGCTT CCATGGTATC AAAGGCAAGA CTGG

35

(2) INFORMATION FOR SEQ ID NO: 279:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

GTCAGGATCC GGTAGTTAAA GTTGGTATTA ACGG

34

(2) INFORMATION FOR SEQ ID NO: 280:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

AGTCAAGCTT GCAATTTTTG CGAAGTATTC CAAGAG

36

(2) INFORMATION FOR SEQ ID NO: 281:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

AGTCGGATCC TTCTTACGAG TTGGGACTGT ATCAAGC

37

(2) INFORMATION FOR SEQ ID NO: 282:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

AGTCAAGCTT GTTTATTTTT TCCTTACTTA CAGATGAAGG

40

(2) INFORMATION FOR SEQ ID NO: 283:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

AGTCGGATCC TACTGAGATG CATCATAATC TAGGAGC

37

(2) INFORMATION FOR SEQ ID NO: 284:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

TCAGCTCGAG TTCTTTGACA TCTCCATCAT AAGTCGC

37

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

GACTGGATCC GGTTTTGAGA AAGTATTGTC AGGGG

35

(2) INFORMATION FOR SEQ ID NO: 286:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

CAGTAAGCTT GGATTTTTTC ATGGATGCAA TTTTTTTGG

39

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

GACTGGATCC GACAACATTT ACTATCCATA CAGTAGAGTC AGC

43

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

GACTAAGCTT GGCATAAGGT TGCAATTCTG GATTAATTGG

40

(2) INFORMATION FOR SEQ ID NO: 289:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

GACTGGATCC GGCTAAGGAA AGAGTGGATG

30

(2) INFORMATION FOR SEQ ID NO: 290:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

GACTAAGCTT TTCATTTTTA AATTGACTAT GCGCCCG

37

(2) INFORMATION FOR SEQ ID NO: 291:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

GACTGGATCC TTGTTCTTAT GAACTTGGTC GTCACC

36

(2) INFORMATION FOR SEQ ID NO: 292:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CATGAAGCTT ATCCTGGATT TTTCCAAGTA AATCT

35

(2) INFORMATION FOR SEQ ID NO: 293:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

GACTGGATCC TTATAAGGGT GAATTAGAAA AAGG

34

(2) INFORMATION FOR SEQ ID NO: 294:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

GACTAAGCTT CTTATTAGGA TTGTTAGTAG TTG

33

(2) INFORMATION FOR SEQ ID NO: 295:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

GACTGGATCC GAATGTTTCAG GCTCAAGAAA GTTCAGG

37

(2) INFORMATION FOR SEQ ID NO: 296:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

a'
cont.

354

GACTAAGCTT TTCCCCTGAT GGAGCAAAGT AATACC

36

(2) INFORMATION FOR SEQ ID NO: 297:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

GACTGGATCC CTTGGGTGTA ACCCATATCC AGCTCCTTCC

40

(2) INFORMATION FOR SEQ ID NO: 298:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

GACTGTCGAC TTCAGCTTGT TTATCTGGGG TTGC

34

(2) INFORMATION FOR SEQ ID NO: 299:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

GACTGGATCC TAGTGATGGT ACTTGGCAAG GAAAACAG

38

(2) INFORMATION FOR SEQ ID NO: 300:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

ACTGCTGCAG ATCTTTGCCA CCTAGCTTCT CATTG

35

(2) INFORMATION FOR SEQ ID NO: 301:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

GTCAGGATCC TGGGATTCAA TATGTCAGAG ATGATACTAG

40

(2) INFORMATION FOR SEQ ID NO: 302:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

CTAGAAGCTT ACGCACCCAT TCACCATTAT CATTTG

35

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

GTCAGGATCC GGATAATAGA GAAGCATTA AAACC

35

(2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AGTCAAGCTT GACAAAATCT TGAAACTCCT CTGGTC

36

(2) INFORMATION FOR SEQ ID NO: 305:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

a'
cont.

GTCAGGATCC AGATTTTGTG GAGGAGTGTC ATACC

35

(2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

AGTCAAGCTT TCCCTTTTTC CCCTTACGAA TCCAGG

36

(2) INFORMATION FOR SEQ ID NO: 307:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

GACTGGATCC ATCTGTAGTT TATGCGGATG AAACACTTAT TAC

43

(2) INFORMATION FOR SEQ ID NO: 308:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

GACTGTCGAC GCTTTGGTAG AGATAGAAGT CATG

34

(2) INFORMATION FOR SEQ ID NO: 309:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

GACTGGATCC TTACTTTGGT ATCGTAGATA CAGCCGGC

38

(2) INFORMATION FOR SEQ ID NO: 310:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

AGTCAAGCTT TGTTAATTGC GTACCTTCTA AGCGACC

37

(2) INFORMATION FOR SEQ ID NO: 311:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

GACTGGATCC AGCTAAGGTT GCATGGGATG CGATTGC

37

(2) INFORMATION FOR SEQ ID NO: 312:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

GACTGTCGAC CTGGGCTTTA TTAGTTTGAC TAGC

34

(2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

CAGTGGATCC CTATCACTAT GTAAATAAAG AGA

33

(2) INFORMATION FOR SEQ ID NO: 314:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

ACTGAAGCTT TTCTGTCCTT GTTTGAGGCA

30

(2) INFORMATION FOR SEQ ID NO: 315:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

CAGTGGATCC TGAGACTCCT CAATCAATAA CAAA

34

(2) INFORMATION FOR SEQ ID NO: 316:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

ACGTAAGCTT ATAATCAGTA GGAGAACTG AACT

34

(2) INFORMATION FOR SEQ ID NO: 317:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

CAGTGGATCC GGATGCTCAA GAAACTGCGG

30

(2) INFORMATION FOR SEQ ID NO: 318:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

GACTAAGCTT TTGCCTCTCA TTCTTGCTTC C

31

(2) INFORMATION FOR SEQ ID NO: 319:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

CAGTGGATCC CGACAAAGGT GAGACTGAG

29

(2) INFORMATION FOR SEQ ID NO: 320:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

ACGTAAGCTT ATTCTTAAT TCAAGTGTTT TCTCTG

36

(2) INFORMATION FOR SEQ ID NO: 321:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GACTGGATCC AAATCAATTG GTAGCACAAG ATCC

34

(2) INFORMATION FOR SEQ ID NO: 322:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

CAGTGTCGAC ATTAGGAGCC ACTGGTCTC

29

(2) INFORMATION FOR SEQ ID NO: 323:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

CAGTGGATCC CAAACAGTCA GCTTCAGGAA C

31

(2) INFORMATION FOR SEQ ID NO: 324:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

GACTCTGCAG TTTAATCTTG TCCCAGGTGG

30

(2) INFORMATION FOR SEQ ID NO: 325:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

GACTGGATCC ATTCGATGAT GCGGATGAAA AG

32

(2) INFORMATION FOR SEQ ID NO: 326:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

GACTAAGCTT CATTTGTCTT TGGGTATTTT CCA

33

(2) INFORMATION FOR SEQ ID NO: 327:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

CAGTGGATCC GGAGAGTCGA TCAAAAGTAG

30

(2) INFORMATION FOR SEQ ID NO: 328:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

GTCACCTGCAG TTGCTCGTCT CGAGGTTC

28

(2) INFORMATION FOR SEQ ID NO: 329:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

CAGTGGATCC ATGGACAACA GGAACTGGG AC

32

(2) INFORMATION FOR SEQ ID NO: 330:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

CAGTAAGCTT ATTAGCTTCT GTACCTGTGT TTG

33

(2) INFORMATION FOR SEQ ID NO: 331:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

GACTGGATCC CGATGGGCTC AATCCAACCC CAGGTCAAGT C

41

(2) INFORMATION FOR SEQ ID NO: 332:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

GACTCTGCAG CATAGCTTTA TCCTCTGACA TCATCGTATC

40

(2) INFORMATION FOR SEQ ID NO: 333:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

GACTGGATCC TTCCAATCAA AAACAGGCAG ATGG

34

(2) INFORMATION FOR SEQ ID NO: 334:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

GACTAAGCTT GAGTCCCATA GTCCAAGGCA

30

(2) INFORMATION FOR SEQ ID NO: 335:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

AGTCGGATCC TATCACAGGA TCGAACGGTA AGACAACC

38

(2) INFORMATION FOR SEQ ID NO: 336:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

ACTGGTCGAC TTCTTTTAAAC TCCGCTACTG TGTC

34

(2) INFORMATION FOR SEQ ID NO: 337:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

CAGTGGATCC AAGTTCATCG AAGATGGTTG GGAAGTCC

38

(2) INFORMATION FOR SEQ ID NO: 338:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

GATCGTCGAC CCGCTCCCAC ATGCTCAACC TT

32

(2) INFORMATION FOR SEQ ID NO: 339:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

TGACGGATCC ATCGCTAGCT AGTGAAATGC AAGAAAG

37

(2) INFORMATION FOR SEQ ID NO: 340:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

TGACAAGCTT ATTCGTTTTT GAACTAGTTG CTTTCGT

37

(2) INFORMATION FOR SEQ ID NO: 341:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

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364

GACTGGATCC GCACCAGATG GGGCACAAGG TTCAGGG

37

(2) INFORMATION FOR SEQ ID NO: 342:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

TGACAAGCTT AACTTGTAAC GAACAGTCA ATCTG

35

(2) INFORMATION FOR SEQ ID NO: 343:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

GACTAGATCT TTTTAACCCA ACTGTTGGTA CTTTCC

36

(2) INFORMATION FOR SEQ ID NO: 344:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TGACAAGCTT GTTAGGTGTT ACATTTTGAC CGTC

34

(2) INFORMATION FOR SEQ ID NO: 345:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

ACTGAGATCT TTTTAACCCA ACTGTTGGTA CTTTC

35

(2) INFORMATION FOR SEQ ID NO: 346:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

GACTAAGCTT TCTACGATAA CGATCATTTT CTTTACC

37

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

GACTGTCGAC TCGTAGATAT TTAAGTCTAA GTGAAGCG

38

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

AGTCAAGCTT GTTAGGTGTT ACATTTTGCA AGTC

34

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

GACTGGATCC CTTTGGTTTT GAAGGAAGTA AG

32

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

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 cont.

368

TGACCTGCAG ACGATTTTGT AAAAATGGAG GTGTATC

37

(2) INFORMATION FOR SEQ ID NO: 351:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

CAGTGGATCC CTACTACCTC TCGAGAGAAA G

31

(2) INFORMATION FOR SEQ ID NO: 352:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

ACTGAAGCTT TTCGCTTTTT ACTCGTTTGA CA

32

(2) INFORMATION FOR SEQ ID NO: 353:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

CAGTGGATCC TAAGGTCAAA AGTCAGACCG CTAAGAAAGT GC

42

(2) INFORMATION FOR SEQ ID NO: 354:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

CAGTAAGCTT TAGGGTATCC AAATACTGGT TGTGTATG

38

(2) INFORMATION FOR SEQ ID NO: 355:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

TGACAGATCT TGACGGGTCT CAGGATCAGA CTCAGG

36

(2) INFORMATION FOR SEQ ID NO: 356:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

TGACAAGCTT CAAAGACATC CACCTCTTGA CCTTTG

36

(2) INFORMATION FOR SEQ ID NO: 357:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

GACTGGATCC TAGAGGCTTT GCCAAATGGT GGGAAGGG

38

(2) INFORMATION FOR SEQ ID NO: 358:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

GTCAGTCGAC TTGTTGTAAC ACTTTTCGAG GTTTGGTACC

40

(2) INFORMATION FOR SEQ ID NO: 359:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CAGTGGATCC TCAAAAAGAG AAGGAAACT TGG

33

(2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

CAGTCTGCAG TTTCTTCAAC AAACCTTGTT CTTG

34

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

CAGTGGATCC ACGTTCTATT GAGGACCACT T

31

(2) INFORMATION FOR SEQ ID NO: 362:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

CAGTAAGCTT TTCCTTCTCA GTCAATCTT TTCC

34

(2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GACTGGATCC CGCTCAAAT ACCAGAGGTG TTCAG

35

(2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

GACTAAGCTT AGTACCATGG GTGTGACAGG TTTGAA

36

(2) INFORMATION FOR SEQ ID NO: 365:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

CTGAGGATCC AATTGTACAA TTAGAAAAAG ATAGC

35

(2) INFORMATION FOR SEQ ID NO: 366:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

TGACAAGCTT GCGTTGACTA GGTTC TGCAA TGCC

34

(2) INFORMATION FOR SEQ ID NO: 367:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

GACTGGATCC TCTGACCAAG CAAAAGAAG CAGTCAATGA

40

(2) INFORMATION FOR SEQ ID NO: 368:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

TCAGCAGCTG ATCATTGACT TTACGATTTG CTCC

34

(2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

GACTGGATCC GTCCGGCTCT GTCCAGTCCA CTTTTCAGC G

41

(2) INFORMATION FOR SEQ ID NO: 370:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TCAGAAGCTT ATTTTGTGTT TCCTTAATGC GTT

33

(2) INFORMATION FOR SEQ ID NO: 371:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

GACTGGATCC GGGACAAATT CAAAAAATA GGCAAGAGG

39

(2) INFORMATION FOR SEQ ID NO: 372:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

GTCAAAGCTT TGGCTCTTTG ATTGCCAACA ACTG

34

(2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

GACTGGATCC TCGCTACCAG CAACAAAGCG AGCAAAAGG

39

(2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

GACTAAGCTT ACTTTTCTCT TTTCCACAC GA

32

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

CAGTGGATCC GAACCGACAA GTCGCCCACT ATCAAGACT

39

(2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

CTGAAAGCTT TGAATTCTCT TTCTTTTCAG GCT

33

(2) INFORMATION FOR SEQ ID NO: 377:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

TCGAGGATCC GGTGTGCGGC TGGCAATATA TCCCGT

36

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

CAGTAAGCTT CCGAACCCAT TCGCCATTAT AGTTGAC

37

(2) INFORMATION FOR SEQ ID NO: 379:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

AGTCGGATCC GGCCAAATCA GAATGGGTAG AAGAC

35

(2) INFORMATION FOR SEQ ID NO: 380:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

TGACCTGCAG CTTCTCATTG ATTTTCATCA TCAC

34

(2) INFORMATION FOR SEQ ID NO: 381:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GACTGGATCC ATTGCAGAT GATTCTGAAG GATGG

35

(2) INFORMATION FOR SEQ ID NO: 382:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

TCAGCTGCAG CTTAACCCAT TCACCATTCT AGTTTAAG

38

(2) INFORMATION FOR SEQ ID NO: 383:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

GACTGGATCC TGTCGCTGCA AATGAACTG AAGTAGC

37

(2) INFORMATION FOR SEQ ID NO: 384:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

GACTAAGCTT ATACCAAACG CTGACATCTA CGCG

34

(2) INFORMATION FOR SEQ ID NO: 385:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

AGTCAGATCT TACGTCTCAG CCTACTTTTG TAAGAGC

37

(2) INFORMATION FOR SEQ ID NO: 386:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

GACTAAGCTT AACCCATTCA CCATTGGCAT TGAC

34

(2) INFORMATION FOR SEQ ID NO: 387:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

CAGTGGATCC TGGACAGGTG AAAGGTCATG CTACATTTGT G

41

(2) INFORMATION FOR SEQ ID NO: 388:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

GACTAAGCTT CAACCATTGA GACCTTGCAA CAC

33

(2) INFORMATION FOR SEQ ID NO: 389:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

GTCAGGATCC GATTGCTCCT TTGAAGGATT TGAGAGAAAC C

41

(2) INFORMATION FOR SEQ ID NO: 390:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GACTAAGCTT CGATCAAAGA TAAGATAAAT ATATATAAAG T

41

(2) INFORMATION FOR SEQ ID NO: 391:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

GACTGGATCC TAGGTCATAT GGGACTTTTT TTCTACAACA AAATAGG

47

(2) INFORMATION FOR SEQ ID NO: 392:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

TGACAAGCTT ATCTATCAGC TCATTTAATC GTTTTTG

37

(2) INFORMATION FOR SEQ ID NO: 393:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

CTGAGGATCC CAACGTTGAG AATTATTGTC GAATG

35

(2) INFORMATION FOR SEQ ID NO: 394:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

TGACAAGCTT GAGTCTACAA AAGTAATGTA C

31

(2) INFORMATION FOR SEQ ID NO: 395:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

GTCAGGATCC CTACTATCAA TCAAGTTCTT CAGCC

35

(2) INFORMATION FOR SEQ ID NO: 396:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

TGACAAGCTT GACTGAGGCT TGGACCAGAT TGAAAAG

37

(2) INFORMATION FOR SEQ ID NO: 397:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

GACTGGATCC GACAAAAACA TTAAACGTC CTGAGG

36

(2) INFORMATION FOR SEQ ID NO: 398:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

GACTAAGCTT AGCACGAACT GTGACGCTGG TTCC

34

(2) INFORMATION FOR SEQ ID NO: 399:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

GACTGGATCC TTCTCAGGAG ACCTTTAAAA ATATC

35

(2) INFORMATION FOR SEQ ID NO: 400:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

GACTAAGCTT GTTGGCCATC TTGTACATAC C

31

(2) INFORMATION FOR SEQ ID NO: 401:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

GACTGGATCC AGTAAATGCG CAATCAAATT C

31

(2) INFORMATION FOR SEQ ID NO: 402:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

AGTCCTGCAG GTATTTAGCC CAATAATCTA TAAAGCT

37

(2) INFORMATION FOR SEQ ID NO: 403:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

CAGTGGATCC TTACCGCGTT CATCAAGATG TC

32

(2) INFORMATION FOR SEQ ID NO: 404:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

GACTAAGCTT GCCAGATGTT GAAAAGAGAG TG

32

(2) INFORMATION FOR SEQ ID NO: 405:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

GACTGGATCC GTGGATGGGC TTAACTATC TTCGTATTCG

40

(2) INFORMATION FOR SEQ ID NO: 406:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

AGTCAAGCTT GCTAGTCTTC ACTTCCCTT TCC

33

(2) INFORMATION FOR SEQ ID NO: 407:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

GACTGTCGAC ACTAAACCAG CATCGTTCGC AGGA

34

(2) INFORMATION FOR SEQ ID NO: 408:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

CTGACTGCAG CTTCTTGAAG AAATAATGAT TGTGG

35

(2) INFORMATION FOR SEQ ID NO: 409:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

CAGTGGATCC TGACTACCTT GAAATCCCAC TT

32

(2) INFORMATION FOR SEQ ID NO: 410:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

CAGTAAGCTT TTTTITAAGG TGTAGAATG ATTCAATC

39

(2) INFORMATION FOR SEQ ID NO: 411:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

CAGTGTGAC TCGTATCTTT TTTTGGAGCA ATGTT

35

(2) INFORMATION FOR SEQ ID NO: 412:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

GACTAAGCTT AAATGTTCCG ATACGGGTGA TTG

33

(2) INFORMATION FOR SEQ ID NO: 413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

CAGTGGATCC GGACTCTCTC AAAGATGTGA AAG

33

(2) INFORMATION FOR SEQ ID NO: 414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

GACTAAGCTT CTTGAGTTTG TCAAGGATTG CTTT

34

(2) INFORMATION FOR SEQ ID NO: 415:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

CAGTGGATCC CAAGAAATCC TATCATCTCT TCCAGAAG

38

(2) INFORMATION FOR SEQ ID NO: 416:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

GACTAAGCTT TTCAGAACTA AAAGCCGCAG CTT

33

(2) INFORMATION FOR SEQ ID NO: 417:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

GACTGGATCC ACGAAATGCA GGCAGACAG

30

(2) INFORMATION FOR SEQ ID NO: 418:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

CAGTAAGCTT ATCAACATAA TCTAGTAAAT AAGCGT

36

(2) INFORMATION FOR SEQ ID NO: 419:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

CAGTGGATCC TGTATAGTTT TTAGCGCTTG TTCTTC

36

(2) INFORMATION FOR SEQ ID NO: 420:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

GTCAAAGCTT TGATAGAGTG TCATAATCTT CTTTAG

36

(2) INFORMATION FOR SEQ ID NO: 421:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

GACTGGATCC GTGTGTCGAG CATATTCTGA AG

32

(2) INFORMATION FOR SEQ ID NO: 422:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

CAGTAAGCTT ACTTTTACCA TTTCTTTGTT CTGCATC

37

(2) INFORMATION FOR SEQ ID NO: 423:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

GACTGTCGAC GTGTTTGGAT AGCATTCAGA ATCAGACG

38

(2) INFORMATION FOR SEQ ID NO: 424:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

CAGTAAGCTT CGGAAGTAAA GACAATTTT CC

32

(2) INFORMATION FOR SEQ ID NO: 425:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

CAGTGGATCC GTGCCTAGAT AGTATTATTA CTCAAAC

37

(2) INFORMATION FOR SEQ ID NO: 426:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

GACTAAGCTT TTTGCTTATT TCTCTCAATT TTTC

34

(2) INFORMATION FOR SEQ ID NO: 427:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

CAGTGGATCC CATTCAGAAG CAGACCTATC AAAATC

36

(2) INFORMATION FOR SEQ ID NO: 428:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

ACTGAAGCTT ATGTAATTTT TTAGATTTT CAATATTTT CAG

43

(2) INFORMATION FOR SEQ ID NO: 429:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

AGTCGGATCC TAAGGCTGAT AATCGTGTTC AAATG

35

(2) INFORMATION FOR SEQ ID NO: 430:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

GACTAAGCTT AAAATTAGAT AGACGTTGAG T

31

(2) INFORMATION FOR SEQ ID NO: 431:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

AGTCGGATCC CTGTGGCAAT CAGTCAGCTG CTTCC

35

(2) INFORMATION FOR SEQ ID NO: 432:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

GACTGTCGAC TTTAATCTTG TCCCAGGTGG TTAATTGACC

40

(2) INFORMATION FOR SEQ ID NO: 433:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

ACTGGTCGAC TTGTCAACAA CAACATGCTA CTTCTGAG

38

(2) INFORMATION FOR SEQ ID NO: 434:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

GACTCTGCAG AAGTTTAACC CACTTATCAT TATCC

35

(2) INFORMATION FOR SEQ ID NO: 435:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

ACTGGGATCC TTGTTCAAGC AAGTCCGTGA CTAGTGAAC

39

(2) INFORMATION FOR SEQ ID NO: 436:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

GACTAAGCTT GGCTAATTCC TTCAAAGTTT GCA

33

(2) INFORMATION FOR SEQ ID NO: 437:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

AGTCGGATCC CTCGCAAATT GAAAAGGCGG CAGTTAGCC

39

(2) INFORMATION FOR SEQ ID NO: 438:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

GACTAAGCTT GTAAATAAGC GTACCTTTTT CTTC

35

(2) INFORMATION FOR SEQ ID NO: 439:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

TCAGGGATCC TTGTCAGTCA GGTTCATATG GTTCTCAG

38

(2) INFORMATION FOR SEQ ID NO: 440:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

AGTCAAGCTT GGCATTGGCG TCGCCGTCCT TC

32

(2) INFORMATION FOR SEQ ID NO: 441:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

GACTGGATCC GGAAACTTCA CAGGATTTTA AAGAGAAG

38

(2) INFORMATION FOR SEQ ID NO: 442:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

GACTGTCGAC AATCAATCCT TCTTCTGCAC TTCT

34

(2) INFORMATION FOR SEQ ID NO: 443:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

CAGTGGATCC TGTGGTCGAA GTTGAGACTC CTCAATC

37

(2) INFORMATION FOR SEQ ID NO: 444:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

GACTAAGCTT TTCTTCAAAT TTATTATCAG C

31

(2) INFORMATION FOR SEQ ID NO: 445:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

AGTCGGATCC AACACCTGTA TATAAAGTTA CAGCAATCG

39

(2) INFORMATION FOR SEQ ID NO: 446:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

GACTGTCGAC TACTTGACCG AATGCGTCGA ATGTACG

37

(2) INFORMATION FOR SEQ ID NO: 447:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

CTGAGGATCC ATTAGACAGA TTAATTGAAA TCGG

34

(2) INFORMATION FOR SEQ ID NO: 448:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

GACTGTCGAC TTAAAGATT GAAGTTTAA AGCT

34

(2) INFORMATION FOR SEQ ID NO: 449:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

388

TGACGGATCC TAAGACAGAT GAACGGAGCA AGGTG

35

(2) INFORMATION FOR SEQ ID NO: 450:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

CTGAAAGCTT TAAGGCTTCC TCAATGAGTT TGTCT

35

(2) INFORMATION FOR SEQ ID NO: 451:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

GACTGGATCC CTGTGAGAAT CAAGCTACAC CCA

33

(2) INFORMATION FOR SEQ ID NO: 452:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

CTGAAAGCTT TTGTAAGTGA GATTGATCTG GGAG

34